

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 17:55:32 ; Search time 92.5 Seconds
(without alignments)
677.353 Million cell updates/sec

Title: NOLAN463-1A.SEQ

Perfect score: 140

Sequence: 1 GAATCAATCATAGTGAAG.....ATATTAGCAGCTGTTAGCC 81

Scoring table:

```

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

```

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/UsPTO.spool.p/NOLAN08728463-1/runat_04082005.125805.24527/app.query.fasta_1.5
-DB=A_Geneseq -QFWT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THRM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN08728463-1.@CGN.1.1.308@runat_04082005.125805.24527 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

```

Database :

```

1: Geneseq16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 113.1 | 80.8 | 249 | 5 | ABP45310 Human Bly |
| 2 | 113.1 | 80.8 | 249 | 7 | ADG96137 Single ch |
| 3 | 93.8 | 67.0 | 250 | 5 | ABP44982 Human Bly |
| 4 | 93.8 | 67.0 | 250 | 7 | ADG95809 Single ch |
| 5 | 93.8 | 67.0 | 253 | 5 | ABP44943 Human Bly |
| 6 | 93.8 | 67.0 | 253 | 7 | ADG95770 Single ch |
| 7 | 92.4 | 66.0 | 80 | 2 | AAW62794 Amino aci |
| 8 | 92.4 | 66.0 | 97 | 2 | AAy05694 Multiple |
| 9 | 92.4 | 66.0 | 97 | 5 | ABG78212 Human Fv |
| 10 | 92.4 | 66.0 | 97 | 5 | ABG91903 Human ant |

| | | | | | | |
|----|------|------|-----|---|----------|------------|
| 11 | 92.4 | 66.0 | 97 | 6 | ABO27107 | Human ger |
| 12 | 92.4 | 66.0 | 97 | 7 | ADB75646 | Human pro |
| 13 | 92.4 | 66.0 | 97 | 7 | ADD28104 | Lymphoma |
| 14 | 92.4 | 66.0 | 97 | 7 | ADF10048 | VEGF anti |
| 15 | 92.4 | 66.0 | 97 | 7 | ADP10150 | Antibody |
| 16 | 92.4 | 66.0 | 97 | 7 | ADF09942 | Antibody |
| 17 | 92.4 | 66.0 | 97 | 7 | ADJ80323 | VH gene 1 |
| 18 | 92.4 | 66.0 | 114 | 3 | ABO1949 | Anti-Id1 |
| 19 | 92.4 | 66.0 | 114 | 3 | ABO1950 | Anti-Id1 |
| 20 | 92.4 | 66.0 | 114 | 3 | ABO1953 | Anti-Id1 |
| 21 | 92.4 | 66.0 | 114 | 3 | ABO1959 | High affi |
| 22 | 92.4 | 66.0 | 114 | 3 | ABO1952 | Anti-Id1 |
| 23 | 92.4 | 66.0 | 114 | 3 | ABO1955 | Streptativ |
| 24 | 92.4 | 66.0 | 114 | 3 | ABO1956 | Streptativ |
| 25 | 92.4 | 66.0 | 114 | 3 | ABO1948 | Wild-type |
| 26 | 92.4 | 66.0 | 114 | 7 | ADG70086 | Diversifi |
| 27 | 92.4 | 66.0 | 114 | 7 | ADG70013 | Diversifi |
| 28 | 92.4 | 66.0 | 115 | 2 | AAr66324 | Human imm |
| 29 | 92.4 | 66.0 | 117 | 4 | AAm60904 | Human bra |
| 30 | 92.4 | 66.0 | 117 | 4 | ABG55317 | Human liv |
| 31 | 92.4 | 66.0 | 117 | 5 | ABG43454 | Human pep |
| 32 | 92.4 | 66.0 | 118 | 6 | ADA89246 | Human ant |
| 33 | 92.4 | 66.0 | 122 | 7 | ADK17418 | Anti-huma |
| 34 | 92.4 | 66.0 | 122 | 8 | ADG42840 | scFv Abl2 |
| 35 | 92.4 | 66.0 | 123 | 2 | AAW03757 | Anti-rhes |
| 36 | 92.4 | 66.0 | 125 | 6 | ADA89266 | Human ant |
| 37 | 92.4 | 66.0 | 125 | 6 | ADA89274 | Human ant |
| 38 | 92.4 | 66.0 | 139 | 3 | AAy99556 | Human Lh1 |
| 39 | 92.4 | 66.0 | 139 | 6 | ABR42859 | Tumour-ep |
| 40 | 92.4 | 66.0 | 139 | 7 | ABW02445 | Human non |
| 41 | 92.4 | 66.0 | 142 | 6 | ABP96287 | Anti-hTNF |
| 42 | 92.4 | 66.0 | 154 | 6 | ABP96293 | Human ant |
| 43 | 92.4 | 66.0 | 190 | 2 | AAy34304 | IGM antib |
| 44 | 92.4 | 66.0 | 202 | 2 | AAy34303 | IGM antib |
| 45 | 92.4 | 66.0 | 205 | 2 | AAy34299 | IGM antib |

ALIGNMENTS

RESULT 1

ABP45310 standard; protein; 249 AA.

AC ABP45310;
XX
DT 19-AUG-2002 (first entry)
DE Human BlyS binding scFv SEQ ID 1321.
XX

Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

OS
PN WO200202641-A1.

PD 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

```

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX Claim 1; Page 1979-1980; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;

Alignment Scores:
Pred. No.: 2.44e-05 Length: 249
Score: 113.10 Matches: 26
Percent Similarity: 20.63% Conservative: 0
Best Local Similarity: 20.63% Mismatches: 1
Query Match: 80.79% Indels: 99
DB: 5 Gaps: 1

NOLAN463-1A.SEQ (1-81) x ABP45310 (1-249)
QY 1 GAAATCAATCATAGTGGAGCAACCACTACACCGCTCCCTCAAGAGT----- 48
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
QY 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
QY 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
QY 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
QY 48 ----- 48
Db 130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
QY 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
QY 64 ATTAGCAGCTGGTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 2
ADG96137
ID ADG96137 standard; protein; 249 AA.
XX
AC ADG96137;
XX

```

```

DT 11-MAR-2004 (first entry)
XX Single chain antibody that immunospecifically binds BlyS SeqID 1321.
XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX Unidentified.
OS WO2003055979-A2.
PN 10-JUL-2003.
XX 14-NOV-2002; 2002WO-US036496.
XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BlyS), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX Example 1; SEQ ID NO 1321; 394pp; English.
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BlyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BlyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiarthritic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BlyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ Sequence 249 AA;

Alignment Scores:
Pred. No.: 2.44e-05 Length: 249
Score: 113.10 Matches: 26
Percent Similarity: 20.63% Conservative: 0
Best Local Similarity: 20.63% Mismatches: 1
Query Match: 80.79% Indels: 99
DB: 7 Gaps: 1

NOLAN463-1A.SEQ (1-81) x ADG96137 (1-249)
QY 1 GAAATCAATCATAGTGGAGCAACCACTACACCGCTCCCTCAAGAGT----- 48
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
QY 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
QY 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
QY 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
QY 48 ----- 48
Db 130 GlySerGlyGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
QY 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
QY 64 ATTAGCAGCTGGTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 2
ADG96137
ID ADG96137 standard; protein; 249 AA.
XX
AC ADG96137;
XX

```

Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
 QY 48 ----- 48
 Db 90 ThrAlaValTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
 QY 48 ----- 48
 Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGly 129
 QY 48 ----- 48
 Db 130 GlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
 QY 49 -----CGGCGCAGTCAGGAT 63
 Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
 QY 64 ATTACGACGCTGTTAGCC 81
 Db 170 IleSerSerTrpLeuAla 175

RESULT 3

ABP44982
 ID ABP44982 standard; protein; 250 AA.

XX AC ABP44982;

XX DT 19-AUG-2002 (first entry)

XX DE Human BlyS binding scFv SEQ ID 993.

XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

XX PT diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 1586-1587; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS

CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 250 AA;

Alignment Scores:
 Pred. No.: 0.00726 Length: 250
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 5 Gaps: 1

NOLAN463-1A.SEQ (1-81) x ABP44982 (1-250)

QY 1 GAATCATCATAGTGGNAGCACCACCACTACACCGTCCCTCAGAGTCGGCG----- 54

Db 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

QY 55 AGTCAGGATATTAGCAGC 72

Db 70 SerGlnAspThrSerAsn 75

RESULT 4

ADG95809

ID ADG95809 standard; protein; 250 AA.

XX AC ADG95809;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds BlyS SeqID 993.

XX KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;

XX KW B cell proliferation; differentiation; scFv; myasthenia gravis;

XX KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

XX KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

XX KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator

XX PT (BlyS), useful for detecting and treating diseases or disorders e.g.

XX PT rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 993; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour

CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BlyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BlyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

XX SQ Sequence 250 AA;

Alignment Scores:
 Pred. No.: 0.00726 Length: 250
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 7 Gaps: 1

NOLAN463-1A.SEQ (1-81) x ADG95809 (1-250)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCTCAAGATCGGGCG----- 54
 Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69
 Qy 55 AGTCAGGATATTAGCAGC 72
 Db 70 SerGlnAspThrSerAsn 75

RESULT 5
 ABP44943

ID ABP44943 standard; protein; 253 AA.

XX AC ABP44943;

XX DT 19-AUG-2002 (first entry)

XX DE Human BlyS binding scFv SEQ ID 954.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Baraah SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.

DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1540-1541; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS in
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 253 AA;

Alignment Scores:
 Pred. No.: 0.00728 Length: 253
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 5 Gaps: 1

NOLAN463-1A.SEQ (1-81) x ABP44943 (1-253)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCTCAAGATCGGGCG----- 54
 Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy 55 AGTCAGGATATTAGCAGC 72

Db 70 SerGlnAspThrSerAsn 75

RESULT 6

ADG95770

ID ADG95770 standard; protein; 253 AA.

XX AC ADG95770;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds BlyS SeqID 954.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;

KW B cell proliferation; differentiation; scFv; myasthenia gravis;

KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

XX WO2003055979-A2.

XX PD 10-JUN-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.


```

PR 19-DEC-2001; 2001US-0340817P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 954; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineoplastic, antiarthritic, neuroprotective,
XX antiinflammatory, antiallergic and cytostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 253 AA;
XX
XX Alignment Scores:
XX Pred. No.: 0.00728 Length: 253
XX Score: 93.80 Matches: 20
XX Percent Similarity: 80.77% Conservative: 1
XX Best Local Similarity: 76.92% Mismatches: 3
XX Query Match: 67.00% Indels: 2
XX DB: 7 Gaps: 1
XX
XX NOLAN463-1A.SEQ (1-81) x ADG95770 (1-253)
XX
XX QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAAGAGTGGCGGCG----- 54
XX 50 GluileAsnHisSerGlySerThrAsnTyraSerProSerLeuAsnSerArgValThrIle 69
XX
XX QY 55 AGTCAGGATATAGCAGC 72
XX 70 SerGlnAspThrSerAsn 75
XX
XX RESULT 7
XX AAW62794
XX ID AAW62794 standard; peptide; 80 AA.
XX
XX AC AAW62794;
XX
XX DT 23-SEP-1998 (first entry)
XX
XX DE Amino acid sequence of a human antibody fragment.
XX
XX KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
XX inactivated endogenous Ig locus; B-cell development;
XX human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
XX kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
XX production; antibody.
XX

```

```

OS Homo sapiens.
XX
XX WO9824893-A2.
XX
XX PD 11-JUN-1998.
XX
XX PF 03-DEC-1997; 97WO-US023091.
XX
XX PR 03-DEC-1996; 96US-00759620.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX WPI; 1998-333314/29.
XX
XX New transgenic non-human mammals - having an inactivated immunoglobulin
XX locus and a near complete human immunoglobulin locus, used for production
XX of human antibodies.
XX
XX Disclosure; Page 71; 128pp; English.
XX
XX AAW62793-822 represent fragments of human antibodies produced by
XX transgenic Xenomice, created using the method of the invention. The
XX specification describes a transgenic non-human mammal which has genome
XX modifications that comprise an inactivated endogenous immunoglobulin (Ig)
XX locus, so that the mammal does not display normal B-cell development. The
XX modified genome also has an inserted human heavy chain Ig locus in
XX germline configuration, the human heavy chain Ig locus comprising a human
XX micro constant region and regulatory and switch sequences, human J-H
XX genes, human D-H genes, and human V-H genes and an inserted human kappa
XX light chain Ig locus in germline configuration, the human kappa light
XX chain Ig locus comprising a human kappa constant region, J-kappa genes,
XX and V-kappa genes, where the number of V-H and V-kappa genes inserted are
XX selected to restore normal B-cell development in the mammal. The
XX transgenic animals have a near complete human Ig locus, including both a
XX human heavy chain locus and a human kappa light chain locus. They can be
XX used for the production of human antibodies when exposed to particular
XX antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
XX will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
XX Sequence 80 AA;
XX
XX Alignment Scores:
XX Pred. No.: 0.00804 Length: 80
XX Score: 92.40 Matches: 19
XX Percent Similarity: 74.07% Conservative: 1
XX Best Local Similarity: 70.37% Mismatches: 1
XX Query Match: 66.00% Indels: 6
XX DB: 2 Gaps: 0
XX
XX NOLAN463-1A.SEQ (1-81) x AAW62794 (1-80)
XX
XX QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAAGAGTGGCGGCGAGTCAG 60
XX 33 GluileAsnHisSerGlySerThrAsnTyraSerProSerLeuAsnSerArgValThr--- 51
XX
XX QY 61 GATATTAGC 69
XX
XX DB 52 ---lleser 53
XX
XX RESULT 8
XX AAY05694
XX ID AAY05694 standard; protein; 97 AA.
XX
XX AC AAY05694;
XX
XX DT 19-JUL-1999 (first entry)
XX
XX DE Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
XX
XX KW Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
XX heavy chain variable region; VH gene; somatic hypermutation;
XX

```

KW B-cell clonality; RA gene; diagnosis; human.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 1. .30
FT /label= FR1
FT
FT Misc-difference 8 /note= "encoded by GGC"
FT
FT Misc-difference 13 /note= "replaces Glu of RA"
FT
FT Misc-difference 14 /note= "encoded by CCT"
FT
FT Misc-difference 23 /note= "replaces Gly of RA"
FT
FT Misc-difference 25 /note= "replaces Phe of RA"
FT
FT Misc-difference 30 /note= "replaces Gly of RA"
FT
FT Region 31. .36
FT /label= CDR1
FT
FT Misc-difference 31 /note= "replaces Gly of RA"
FT
FT Misc-difference 32 /note= "replaces Phe of RA"
FT
FT Region 37. .50
FT /label= FR2
FT
FT Region 51. .66
FT /label= CDR2
FT
FT Misc-difference 56 /note= "replaces Asn of RA"
FT
FT Misc-difference 57 /note= "replaces Ser of RA"
FT
FT Misc-difference 58 /note= "replaces Lys of RA"
FT
FT Region 67. .97
FT /label= FR3
FT
FT Misc-difference 71 /note= "replaces Leu of RA"
FT
FT Misc-difference 81 /note= "replaces Arg of RA"
FT
FT
XX WO9915696-A1.
XX
XX 01-APR-1999.
XX
XX 17-SEP-1998; 98WO-CA000873.
XX
XX 19-SEP-1997; 97CA-02216595.
XX
XX 04-NOV-1997; 97CA-02220245.
XX
XX (QINY/) QIN Y.
XX
XX Qin Y;
XX
XX WPI; 1999-276985/23.
XX
XX N-PSDB; AAX25318.
XX
XX Determination of B-cell clonality by amplification or enzymatic digestion.
XX
XX Disclosure; Fig 9D; 67pp; English.
XX
XX This sequence represents a heavy chain variable region (VH) as predicted from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19). Differences in nucleotide and predicted amino acid (see AAX05691-94) sequences were compared with the closest known germline VH genes; for 4d76, this was RA. The results provided direct evidence that intrathecal clonally expanded B-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that have undergone antigen selection. This finding implicates an important pathogenic pathway for

CC the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
XX
SQ Sequence 97 AA;

Alignment Scores:
Pred. No.: 0.00847 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x AAY05694 (1-97)

Qy 1 GAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluileasnhisserGlyserThrAsnTyzAsnProserLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 9
ABG78212
ID ABG78212 standard; protein; 97 AA.
XX AC ABG78212;
XX
XX 15-NOV-2002 (first entry)
XX Human Fv molecule hypervariable region related peptide #87.
XX
XX Human Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
XX Homo sapiens.
XX
XX WO200259264-A2.
XX
XX 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US049440.
XX
XX 29-DEC-2000; 2000US-00751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX Hegai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX Plaksin D, Peretz T;
XX
XX WPI; 2002-619166/66.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other cells.
XX
XX Claim 13; Page 193; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a CC composition for use in inhibiting the growth of a diseased or cancer CC cell. This sequence represents a human Fv molecule hypervariable region CC related peptide of the invention

XX Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.00847 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 5 Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABG78212 (1-97)

QY 1 GAATCAATCATAGTGGAGCACCACCACTACACCGTCCCTCAAGAGTCGGCGAGTCAG 60
 |||||
 Db 50 GlulleAsnHisSerGlySerThrAsnTyxRanProSerLeuLysSerArgValThr--- 68
 QY 61 GATATTAGC 69
 |||||
 Db 69 ---IleSer 70

RESULT 10

ABG91903

ID ABG91903 standard; protein; 97 AA.

XX

AC ABG91903;

DT 04-DEC-2002 (first entry)

XX Human antibody fragment #87.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

OS WO200253700-A2.

PN 11-JUL-2002.

PD 31-DEC-2001; 2001WO-US049442.

PF 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Sznathon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

DR Novel isolated epitope present on cancer cells and important in

XX physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

PT diseases, and cancer.

XX Disclosure; Page 269; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one

CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.00847 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 5 Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABG91903 (1-97)

QY 1 GAATCAATCATAGTGGAGCACCACCACTACACCGTCCCTCAAGAGTCGGCGAGTCAG 60
 |||||
 Db 50 GlulleAsnHisSerGlySerThrAsnTyxRanProSerLeuLysSerArgValThr--- 68

QY 61 GATATTAGC 69
 |||||

Db 69 ---IleSer 70

RESULT 11

ABO27107

ID ABO27107 standard; protein; 97 AA.

XX

AC ABO27107;

DT 10-SEP-2003 (first entry)

XX Human germline heavy chain variable region gene segment #40.

XX Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.

XX Homo sapiens.

OS US2003039649-A1.

PN 27-FEB-2003.

PD 12-JUL-2002; 2002US-00194975.

PF 12-JUL-2001; 2001US-0305111P.

XX (FOOT/) FOOTE J.

XX Foote J;

XX WPI; 2003-492151/46.

XX Making humanized antibody for converting antibody, by making chimeric
 PT antibodies containing complementarity determining region from non-human
 PT antibody and appropriate framework sequences of human antibodies.

XX Example 1; Fig 1; 31pp; English.

XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX
 SQ Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.00847 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 6 Gaps: 0

NOLAN463-1A.SEQ (1-81) x ABO27107 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCCCTCAAGAGTCGGCGAGTCAG 60
 Db |||||
 50 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
 Db |||||
 69 ---IleSer 70

RESULT 12
 ADB75646
 ID ADB75646 standard; protein; 97 AA.
 XX
 AC ADB75646;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 DE Human protein relating to the invention SEQ ID NO:55.
 XX
 XX antibody library; CD1 region; CD2 region; VH region; VL region;
 KW immunoglobulin; CD3 region; TM1 scFv; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003041198-A1.
 XX
 XX 30-MAY-2003.
 XX
 XX 22-NOV-2002; 2002WO-JP012236.
 XX
 XX 22-NOV-2001; 2001JP-00358602.
 XX
 XX (UYKE-) UNIV KEIO.
 XX

PI Shimizu N, Takayanagi A, Okui M;
 XX
 DR WPI; 2003-449818/42.
 XX
 XX Highly stable artificial antibody libraries with super-repertoire and

PT little contamination from unexpressible ones, useful as tool in
 XX proteomics and e.g. for diagnosis and treating various diseases.
 XX
 PS Disclosure; Page 101; 108pp; Japanese.
 XX
 CC The invention relates to a novel artificial single-stranded antibody
 CC library with super-repertoire. The library is created by using a cDNA
 CC library as template for amplifying a fragment containing the CD1 and CD2
 CC regions of the VH or VL region of immunoglobulin gene and a fragment
 CC containing the CD3 region by PCR, respectively, producing VH and VL
 CC libraries, transferring into a host, and displaying the single-stranded
 CC antibody on a phage surface. An antibody library of the invention is
 CC useful as a tool in proteomics and antibody chips and filters, for
 CC screening ligands for antigens, and for studying protein-DNA interaction,
 CC diagnosis and treating various diseases. The present sequence represents
 CC a protein of the invention.
 XX

SQ Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.00847 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 7 Gaps: 0

NOLAN463-1A.SEQ (1-81) x ADB75646 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCCCTCAAGAGTCGGCGAGTCAG 60
 Db |||||
 50 GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
 Db |||||
 69 ---IleSer 70

RESULT 13
 ADD28104
 ID ADD28104 standard; protein; 97 AA.
 XX
 AC ADD28104;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 DE Lymphoma related immunoglobulin variable region F5.
 XX

KW B-cell; malignant; immunoglobulin; immunoglobulin variable region;
 KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
 KW cytostatic; gene therapy; glycosylation inhibitor;
 KW non-Hodgkin's lymphoma.
 XX

OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003074059-A2.
 XX
 XX 12-SEP-2003.
 XX
 XX 24-FEB-2003; 2003WO-GB000783.
 XX
 XX 07-MAR-2002; 2002GB-00005395.
 XX
 XX (CANC-) CANCER RES TECHNOLOGY LTD.
 XX

XX Zhu D, Stevenson F;
 XX
 XX WPI; 2003-902720/82.
 XX

XX Classifying a B-cell as malignant or normal by isolating a sequence
 PT representing an Ig variable region from the B cell, detecting the
 PT presence of a glycosylation site and classifying the cell as malignant or
 PT normal.

XX Disclosure; Fig 4; 61pp; English.

XX The present invention describes a method for classifying a B-cell as

CC malignant or normal comprising: (a) isolating a sequence representing an

CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the

CC presence of a glycosylation site; and (c) classifying the cell as

CC malignant or normal on the basis of the presence or absence of a

CC glycosylation site. Also described: (1) treating a patient suffering from

CC or at risk of having lymphoma; (2) screening for substances capable of

CC inhibiting glycosylation of the Ig variable region of the B cell receptor

CC ; and (3) screening for substances (S) capable of inhibiting the

CC interaction between lectins of the type found in the germinal centre and

CC N-glycans found on the surface of Ig of lymphoma cells. (S) has

CC cytosstatic activity, and can be used in gene therapy, and as a

CC glycosylation inhibitor. The method is useful in classifying a B-cell as

CC malignant or normal. The glycosylation inhibitor is useful in preparing a

CC medicament for treating non-Hodgkin's lymphoma. The present sequence

CC represents an Ig variable region sequence which is used in the

CC exemplification of the present invention.

XX

SQ Sequence 97 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00847 | Length: | 97 |
| Score: | 92.40 | Matches: | 19 |
| Percent Similarity: | 74.07% | Conservative: | 1 |
| Best Local Similarity: | 70.37% | Mismatches: | 1 |
| Query Match: | 66.00% | Indels: | 6 |
| DB: | 7 | Gaps: | 0 |

NOLAN463-1A.SEQ (1-81) x ADD28104 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
|||
Db 50 GlulleasnHISerGlySerThrAsnTyAsnProSerLeuLySerArgValThr--- 68
|||
Qy 61 GATATTAGC 69
|||
Db 69 ---IleSer 70

RESULT 14

ADF10048

ID ADF10048 standard; protein; 97 AA.

XX

AC ADF10048;

XX

XX

DT 12-FEB-2004 (first entry)

XX

XX VEGF antibody heavy chain variable region VH_4-34.

XX

DE Antibody; stability; solubility; antigen binding affinity;

XX

KW variable region; human; VEGF.

XX

OS Homo sapiens.

XX

XX WO2003074679-A2.

XX

XX

XX

PD 12-SEP-2003.

XX

XX

PF 03-MAR-2003; 2003WO-US006598.

XX

XX

PR 01-MAR-2002; 2002US-0360843P.

XX

PR 29-MAY-2002; 2002US-0384197P.

XX

XX

PA (XENC-) XENCOR.

XX

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX

XX WPI; 2003-722066/68.

XX

XX Computer optimization of physicochemical properties of antibodies

PT comprises analyzing the interactions of amino acids at variable

PT positions.

XX

PS Example 6; Fig 16a; 135pp; English.

XX

CC The present invention relates to a method for optimizing at least one

CC physico-chemical property of an antibody by a computational screening

CC method. The method comprises: receiving a template antibody structure;

CC selecting at least one variable position belonging to the antibody

CC structure; selecting at least one amino acid to be considered at the

CC variable position(s); analyzing the interaction of each selected amino

CC acid at each variable position with at least part of the remainder of the

CC antibody, including the selected amino acids at other variable positions;

CC and identifying a set of at least one antibody sequence with at least one

CC optimized physico-chemical property. The method is useful for optimizing

CC the physico-chemical properties of an antibody, especially the stability,

CC solubility, or antigen binding affinity. The optimized antibody may be

CC useful for treating a patient. The present sequence is an antibody

CC variable region sequence used to illustrate the invention.

XX

SQ Sequence 97 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00847 | Length: | 97 |
| Score: | 92.40 | Matches: | 19 |
| Percent Similarity: | 74.07% | Conservative: | 1 |
| Best Local Similarity: | 70.37% | Mismatches: | 1 |
| Query Match: | 66.00% | Indels: | 6 |
| DB: | 7 | Gaps: | 0 |

NOLAN463-1A.SEQ (1-81) x ADF10048 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
|||
Db 50 GlulleasnHISerGlySerThrAsnTyAsnProSerLeuLySerArgValThr--- 68
|||
Qy 61 GATATTAGC 69
|||
Db 69 ---IleSer 70

RESULT 15

ADF10150

ID ADF10150 standard; protein; 97 AA.

XX

AC ADF10150;

XX

XX

DT 12-FEB-2004 (first entry)

XX

XX Antibody heavy chain variable region VH_4-34.

XX

DE Antibody; stability; solubility; antigen binding affinity;

XX

KW variable region; human.

XX

OS Homo sapiens.

XX

XX WO2003074679-A2.

XX

XX

XX

PD 12-SEP-2003.

XX

XX

PF 03-MAR-2003; 2003WO-US006598.

XX

XX

PR 01-MAR-2002; 2002US-0360843P.

XX

PR 29-MAY-2002; 2002US-0384197P.

XX

XX

PA (XENC-) XENCOR.

XX

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX

XX WPI; 2003-722066/68.

XX

XX Computer optimization of physicochemical properties of antibodies

PT comprises analyzing the interactions of amino acids at variable

XX

PS Example 16; Fig 40a; 135pp; English.

XX The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.

XX SQ Sequence 97 AA;

Alignment Scores:
Pred. No.: 0.00847 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 7 Gaps: 0

NOLAN463-1A.SEQ (1-81) x ADF10150 (1-97)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCTCAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db |||||
50 GluileAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db |||||
69 ---IleSer 70

Search completed: August 4, 2005, 18:14:24
Job time : 97.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:05:28 ; Search time 23.25 Seconds
(without alignments)
520.135 Million cell updates/sec

Title: NOLAN463-1A.SEQ

Perfect score: 140

Sequence: 1 GAATTCATCATAGTGGAG.....ATATTAGAGCTGTTAGCC 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cg2_1/USPTO.spool/p/NOLAN08728463-1/runat_04082005_125807_24557/app_query.fasta_1.5
-DB=Issued Patents AA -QFWT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pcp -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1.1 66 @runat_04082005_125807_24557 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

Issued Patents AA:*
1: /cg2_6/ptodata/1/iaa/5A.COMB.pcp:*
2: /cg2_6/ptodata/1/iaa/5B.COMB.pcp:*
3: /cg2_6/ptodata/1/iaa/6A.COMB.pcp:*
4: /cg2_6/ptodata/1/iaa/6B.COMB.pcp:*
5: /cg2_6/ptodata/1/iaa/PTCUS.COMB.pcp:*
6: /cg2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 92.4 | 66.0 | 116 | 3 | US-08-545-809A-118 |
| 2 | 92.4 | 66.0 | 123 | 3 | Sequence 118, Appl |
| 3 | 92.4 | 66.0 | 139 | 4 | Sequence 4, Appl |
| 4 | 92.4 | 66.0 | 472 | 3 | Sequence 2, Appl |
| 5 | 87.4 | 62.4 | 429 | 4 | Sequence 8, Appl |
| 6 | 84.4 | 60.3 | 118 | 3 | Sequence 6, Appl |
| 7 | 84.4 | 60.3 | 118 | 4 | Sequence 25, Appl |
| 8 | 84.4 | 60.3 | 118 | 4 | Sequence 25, Appl |
| 9 | 84.4 | 60.3 | 118 | 4 | Sequence 25, Appl |
| 10 | 81 | 57.9 | 120 | 3 | Sequence 137, Appl |
| 11 | 80.7 | 57.6 | 130 | 3 | Sequence 5, Appl |
| 12 | 80.7 | 57.6 | 130 | 3 | Sequence 5, Appl |

| | | | | | | |
|----|------|------|-----|---|--------------------|--------------------|
| 13 | 80.7 | 57.6 | 130 | 4 | US-08-802-096-5 | Sequence 5, Appl |
| 14 | 80.7 | 57.6 | 130 | 4 | US-08-802-077-5 | Sequence 5, Appl |
| 15 | 79.4 | 56.7 | 147 | 4 | US-09-471-276-835 | Sequence 835, Appl |
| 16 | 79.4 | 56.7 | 447 | 4 | US-09-372-425A-2 | Sequence 2, Appl |
| 17 | 77 | 55.0 | 119 | 2 | US-08-428-197-16 | Sequence 16, Appl |
| 18 | 77 | 55.0 | 119 | 5 | PCT-US93-10555-16 | Sequence 16, Appl |
| 19 | 76.4 | 54.6 | 112 | 3 | US-09-344-587-14 | Sequence 14, Appl |
| 20 | 75.9 | 54.2 | 118 | 2 | US-08-652-816A-13 | Sequence 13, Appl |
| 21 | 74.4 | 53.1 | 120 | 4 | US-09-424-840B-20 | Sequence 20, Appl |
| 22 | 73.4 | 52.4 | 21 | 3 | US-08-918-148-45 | Sequence 45, Appl |
| 23 | 73.4 | 52.4 | 21 | 4 | US-09-138-091A-45 | Sequence 45, Appl |
| 24 | 73.4 | 52.4 | 76 | 3 | US-08-851-362D-22 | Sequence 22, Appl |
| 25 | 73.4 | 52.4 | 96 | 3 | US-08-851-362D-35 | Sequence 35, Appl |
| 26 | 73.4 | 52.4 | 116 | 3 | US-08-545-809A-140 | Sequence 140, Appl |
| 27 | 73.4 | 52.4 | 117 | 3 | US-08-851-362D-48 | Sequence 48, Appl |
| 28 | 73.4 | 52.4 | 118 | 3 | US-08-545-809A-142 | Sequence 142, Appl |
| 29 | 73.4 | 52.4 | 119 | 3 | US-09-025-769B-39 | Sequence 39, Appl |
| 30 | 73.4 | 52.4 | 119 | 3 | US-09-025-769B-65 | Sequence 65, Appl |
| 31 | 73.4 | 52.4 | 119 | 4 | US-09-490-070A-39 | Sequence 39, Appl |
| 32 | 73.4 | 52.4 | 119 | 4 | US-09-490-070A-65 | Sequence 65, Appl |
| 33 | 73.4 | 52.4 | 119 | 4 | US-09-490-153-39 | Sequence 39, Appl |
| 34 | 73.4 | 52.4 | 119 | 4 | US-09-490-153-65 | Sequence 65, Appl |
| 35 | 73.4 | 52.4 | 119 | 4 | US-09-490-324-39 | Sequence 39, Appl |
| 36 | 73.4 | 52.4 | 119 | 4 | US-09-490-324-65 | Sequence 65, Appl |
| 37 | 73.4 | 52.4 | 139 | 4 | US-09-471-276-837 | Sequence 837, Appl |
| 38 | 73.4 | 52.4 | 244 | 3 | US-08-918-148-79 | Sequence 79, Appl |
| 39 | 73.4 | 52.4 | 244 | 4 | US-09-138-091A-77 | Sequence 77, Appl |
| 40 | 73 | 52.1 | 100 | 4 | US-09-726-219A-169 | Sequence 169, Appl |
| 41 | 72.4 | 51.7 | 140 | 4 | US-09-471-276-850 | Sequence 850, Appl |
| 42 | 72.4 | 51.7 | 240 | 2 | US-07-956-399-2 | Sequence 2, Appl |
| 43 | 72 | 51.4 | 95 | 4 | US-09-471-276-882 | Sequence 882, Appl |
| 44 | 72 | 51.4 | 116 | 3 | US-08-545-809A-92 | Sequence 92, Appl |
| 45 | 72 | 51.4 | 119 | 3 | US-08-767-128-18 | Sequence 18, Appl |

ALIGNMENTS

RESULT 1

US-08-545-809A-118
; Sequence 118, Application US/08545809A
; Patent No. 6096878

GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku

; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street
; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A

; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

```
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.: 0.000752 Length: 116
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 3 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-545-809A-118 (1-116)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAACCCGTCCTCAAGAGTCGGCGGAGTCAG 60
Db 69 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 87
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793.450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-4
```

```
Alignment Scores:
Pred. No.: 0.000768 Length: 123
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 3 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-793-450-4 (1-123)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAACCCGTCCTCAAGAGTCGGCGGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:
Pred. No.: 0.000802 Length: 139
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-203-768A-2 (1-139)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAACCCGTCCTCAAGAGTCGGCGGAGTCAG 60
Db 69 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 87
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
```



```
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-793-450-8

Alignment Scores:
Pred. No.: 0.00124 Length: 472
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 3 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-793-450-8 (1-472)

Qy 1 GAATCAATCATAGTGAAGCACCACCACTACACCGCTCCCTCAAGAGTCGGCGGAGTCAG 60
Db 69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 5
US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Heavy chain without Tailpiece - AA
; US-09-372-425A-6

Alignment Scores:
Pred. No.: 0.00554 Length: 429
Score: 87.40 Matches: 18
Percent Similarity: 74.07% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 62.43% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-372-425A-6 (1-429)

Qy 1 GAATCAATCATAGTGAAGCACCACCACTACACCGCTCCCTCAAGAGTCGGCGGAGTCAG 60
Db 69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 6
US-09-025-769B-25
; Sequence 25, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-25
Alignment Scores:
Pred. No.: 0.00872 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservatives: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 3 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-025-769B-25 (1-118)
Qy 1 GAAATCAATCATGTGGAGCACCACTACAAACCGTCCTCAAGAGTCGGGCGAGTCAG 60
Db 50 GluileTyHisSerGlySerThrAsnTyAsnProSerLeuLySerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25
Alignment Scores:
Pred. No.: 0.00872 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservatives: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-490-070A-25 (1-118)
Qy 1 GAAATCAATCATGTGGAGCACCACTACAAACCGTCCTCAAGAGTCGGGCGAGTCAG 60
Db 50 GluileTyHisSerGlySerThrAsnTyAsnProSerLeuLySerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
```

Alignment Scores: 0.00872 Length: 118
Pred. No.: 84.40 Matches: 18
Score: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-490-153-25 (1-118)

Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
|||

Qy 61 GATATTAGC 69
|||||
Db 69 ---IleSer 70
|||

RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores: 0.00872 Length: 118
Pred. No.: 84.40 Matches: 18
Score: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2

Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-490-324-25 (1-118)

Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
|||

Qy 61 GATATTAGC 69
|||||
Db 69 ---IleSer 70
|||

RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiro
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-137

Alignment Scores: 0.0248 Length: 120
Pred. No.: 81.00 Matches: 15
Score: 79.17% Conservative: 4
Best Local Similarity: 62.50% Mismatches: 5
Query Match: 57.86% Indels: 0
DB: 3 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-08-545-809A-137 (1-120)

Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 69 GlulleHisSerGlySerThrTyrAsnProSerLeuLysSerArgIleThrMet 88
|||

Qy 61 GATATTAGCAGC 72
|||

```
Db      89 SerValAspThr 92

RESULT 11
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-151-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

Qy      70 -----AGCTGGTTA 78
Db      92 AlaThrTyTrCysAlaIrrpVal 99

RESULT 12
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

Qy      70 -----AGCTGGTTA 78
Db      92 AlaThrTyTrCysAlaIrrpVal 99

RESULT 13
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
```

```
Db      89 SerValAspThr 92

RESULT 11
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-151-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

Qy      70 -----AGCTGGTTA 78
Db      92 AlaThrTyTrCysAlaIrrpVal 99

RESULT 12
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 2
Gaps: 2
DB: 3

NOLAN463-1A.SEQ (1-81) x US-08-466-163B-5 (1-130)

Qy      4 ATCAATCATAGTGGAGACCAACTACAAACCGTCCCTCAAGAGTCGGCGAGT----- 57
Db      52 IleaShHisSerGlyThrThrSerTyraSnProSerLeuLySerArgIleSerIleThr 71
Qy      58 CAGGATATTAGC----- 69
Db      72 ArgAspThrSerLyAsnGlnPheLeuGlnLeuAenSerValThrThrGluAspThr 91

Qy      70 -----AGCTGGTTA 78
Db      92 AlaThrTyTrCysAlaIrrpVal 99

RESULT 13
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
```

; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:

Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 2
Query Match: 57.64% Indels: 23
DB: 4 Gaps: 2

NOLAN463-1A.SEQ (1-81) x US-09-802-096-5 (1-130)

Qy 4 ATCAATCATAGTGAAGACCACTACACCGCTCCCTCAAGAGTCGGCGAGT----- 57

Db 52 lIeaSHISerGlyThrSerTyrAsnProSerLeuYsSerArgIleSerIleThr 71

Qy 58 CAGGATATTAGC----- 69

Db 72 ArgAspThrSerLySAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy 70 -----AGCTGGTTA 78

Db 92 AlathrTyrTyrCysAlaTIpVal 99

RESULT 14

US-09-802-077-5

; Sequence 5, Application US/09802077

; Patent No. 6699472

; GENERAL INFORMATION:

; APPLICANT: Presta, Paula M.

; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

; FILE REFERENCE: P07182C2US

; CURRENT APPLICATION NUMBER: US/09/802,077

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-802-077-5

Alignment Scores:

Pred. No.: 0.028 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 2
Query Match: 57.64% Indels: 23
DB: 4 Gaps: 2

NOLAN463-1A.SEQ (1-81) x US-09-802-077-5 (1-130)

Qy 4 ATCAATCATAGTGAAGACCACTACACCGCTCCCTCAAGAGTCGGCGAGT----- 57

Db 52 lIeaSHISerGlyThrSerTyrAsnProSerLeuYsSerArgIleSerIleThr 71

Qy 58 CAGGATATTAGC----- 69

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-802-077-5

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-802-077-5

Db 72 ArgAspThrSerLySAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91
Qy 70 -----AGCTGGTTA 78
Db 92 AlathrTyrTyrCysAlaTIpVal 99

RESULT 15

US-09-471-276-835

; Sequence 835, Application US/09471276

; Patent No. 6822072

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6822072

; FILE REFERENCE: GENSET.025CPI

; CURRENT APPLICATION NUMBER: US/09/471,276

; CURRENT FILING DATE: 1999-12-21

; EARLIER APPLICATION NUMBER: 09/057,719

; EARLIER FILING DATE: 1998-04-09

; EARLIER APPLICATION NUMBER: 09/069,047

; EARLIER FILING DATE: 1998-04-28

; EARLIER APPLICATION NUMBER: PCT/IB99/00712

; EARLIER FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 1622

; SOFTWARE: Patent.pm

; SEQ ID NO 835

; LENGTH: 147

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -26...-1

US-09-471-276-835

Alignment Scores:

Pred. No.: 0.0435 Length: 147
Score: 79.40 Matches: 16
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 59.26% Mismatches: 3
Query Match: 56.71% Indels: 6
DB: 4 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-09-471-276-835 (1-147)

Qy 1 GAATCAATCATAGTGAAGACCACTACACCGCTCCCTCAAGAGTCGGCGAGTCAG 60

Db 77 GlulleAspHisGlyGlyAenThrAsnProSerLeuYsSerArgVal***---- 95

Qy 61 GATATTAGC 69

Db 96 ---IleSer 97

Search completed: August 4, 2005, 18:23:03

Job time : 25.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:20:25 ; Search time 80.25 Seconds
(without alignments)
788.093 Million cell updates/sec

Title: NOLAN463-1A.SEQ

Perfect score: 140

Sequence: 1 GAATCATCATAGTGGAG.....ATATTAGAGCTGTTAGCC 81

Scoring table:

| | BLOSUM62 | Xgapop 10.0 | Xgapext 0.1 |
|-------------|----------|-------------|-------------|
| Ygapop 10.0 | | | 0.1 |
| Ygapext 0.1 | | | 0.1 |
| Fgapop 6.0 | | | 0.1 |
| Delop 6.0 | | | 0.1 |

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/p/NOLAN08728463-1/runat_04082005_125809_24629/app_query.fasta_1.5
-DB=Published Applications AA -QFMT=fastan -SUFRFX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000
-USER=NOLAN08728463-1 @CIGN 1.1 260 @runat_04082005_125809_24629 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 113.1 | 80.8 | 249 | 10 | US-09-880-748-1321 |
| 2 | 113.1 | 80.8 | 249 | 15 | US-10-293-418-1321 |
| 3 | 96.4 | 68.9 | 115 | 17 | US-10-898-408-12 |
| 4 | 93.8 | 67.0 | 250 | 10 | US-09-880-748-993 |
| 5 | 93.8 | 67.0 | 250 | 15 | US-10-293-418-993 |
| 6 | 93.8 | 67.0 | 253 | 10 | US-09-880-748-954 |
| 7 | 93.8 | 67.0 | 253 | 15 | US-10-293-418-954 |
| 8 | 92.4 | 66.0 | 80 | 14 | US-10-078-958-2 |
| 9 | 92.4 | 66.0 | 97 | 14 | US-10-194-875-40 |
| 10 | 92.4 | 66.0 | 97 | 15 | US-10-308-817-83 |
| 11 | 92.4 | 66.0 | 97 | 15 | US-10-032-038B-87 |
| 12 | 92.4 | 66.0 | 97 | 15 | US-10-029-988B-87 |
| 13 | 92.4 | 66.0 | 97 | 15 | US-10-032-423A-87 |
| 14 | 92.4 | 66.0 | 97 | 15 | US-10-453-698-83 |
| 15 | 92.4 | 66.0 | 97 | 15 | US-10-029-926B-87 |
| 16 | 92.4 | 66.0 | 97 | 16 | US-10-379-392-47 |
| 17 | 92.4 | 66.0 | 114 | 17 | US-10-733-532-128 |
| 18 | 92.4 | 66.0 | 117 | 9 | US-09-864-761-44315 |
| 19 | 92.4 | 66.0 | 118 | 15 | US-10-371-942-90 |
| 20 | 92.4 | 66.0 | 118 | 17 | US-10-893-576-192 |
| 21 | 92.4 | 66.0 | 122 | 15 | US-10-360-828-63 |
| 22 | 92.4 | 66.0 | 125 | 15 | US-10-371-942-110 |
| 23 | 92.4 | 66.0 | 125 | 15 | US-10-371-942-118 |
| 24 | 92.4 | 66.0 | 139 | 14 | US-10-300-675-2 |
| 25 | 92.4 | 66.0 | 139 | 17 | US-10-310-124-2 |
| 26 | 92.4 | 66.0 | 139 | 17 | US-10-893-576-43 |
| 27 | 92.4 | 66.0 | 142 | 17 | US-10-484-790A-10 |
| 28 | 92.4 | 66.0 | 223 | 10 | US-09-972-656-66 |
| 29 | 92.4 | 66.0 | 229 | 10 | US-09-972-656-82 |
| 30 | 92.4 | 66.0 | 230 | 10 | US-09-972-656-72 |
| 31 | 92.4 | 66.0 | 249 | 10 | US-09-880-748-957 |
| 32 | 92.4 | 66.0 | 249 | 15 | US-10-293-418-957 |
| 33 | 92.4 | 66.0 | 250 | 10 | US-09-880-748-1413 |
| 34 | 92.4 | 66.0 | 250 | 15 | US-10-293-418-1413 |
| 35 | 92.4 | 66.0 | 253 | 10 | US-09-880-748-1333 |
| 36 | 92.4 | 66.0 | 253 | 15 | US-10-293-418-1333 |
| 37 | 92.4 | 66.0 | 254 | 10 | US-09-880-748-1659 |
| 38 | 92.4 | 66.0 | 254 | 15 | US-10-293-418-1659 |
| 39 | 92.4 | 66.0 | 450 | 17 | US-10-484-790A-17 |
| 40 | 92.4 | 66.0 | 453 | 17 | US-10-484-790A-18 |
| 41 | 90.4 | 64.6 | 246 | 10 | US-09-880-748-1847 |
| 42 | 90.4 | 64.6 | 246 | 15 | US-10-293-418-1847 |
| 43 | 90.3 | 64.5 | 123 | 14 | US-10-269-805-31 |
| 44 | 90.3 | 64.5 | 123 | 14 | US-10-269-805-55 |
| 45 | 88.4 | 63.1 | 255 | 10 | US-09-880-748-1642 |

ALIGNMENTS

RESULT 1

US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US20030055937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

```
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.: 3.33e-05 Length: 249
Score: 113.10 Matches: 26
Percent Similarity: 20.63% Conservative: 0
Best Local Similarity: 20.63% Mismatches: 1
Query Match: 80.79% Indels: 99
DB: 10 Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-09-880-748-1321 (1-249)
Qy 1 GAATCAATCATAGTGGAGCACCACCACTACACCGCTCCCTCAGAGT----- 48
Db 50 GluileasnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
Qy 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
Qy 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
Qy 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGly 129
Qy 48 ----- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
Qy 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
Qy 64 ATTAGCAGCTGGTTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 2
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF52392
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321

Alignment Scores:
Pred. No.: 3.33e-05 Length: 249
Score: 113.10 Matches: 26
Percent Similarity: 20.63% Conservative: 0
Best Local Similarity: 20.63% Mismatches: 1
Query Match: 80.79% Indels: 99
DB: 15 Gaps: 1

NOLAN463-1A.SEQ (1-81) x US-10-293-418-1321 (1-249)
Qy 1 GAATCAATCATAGTGGAGCACCACCACTACACCGCTCCCTCAGAGT----- 48
Db 50 GluileasnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
Qy 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
Qy 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
Qy 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGly 129
Qy 48 ----- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
Qy 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
Qy 64 ATTAGCAGCTGGTTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 3
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; APPLICANT: YAN, Wei
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.: 0.00362 Length: 115
Score: 96.40 Matches: 19
Percent Similarity: 41.18% Conservative: 2
Best Local Similarity: 37.25% Mismatches: 4
Query Match: 68.86% Indels: 26
DB: 17 Gaps: 1
```



```
NOLAN463-1A.SEQ (1-81) x US-10-898-408-12 (1-115)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCTCAAGAGTCGGCGAGTCAG 60
    |||||
Db 50 GluileAenHisSerGlySerThrAsnTyrAsnProSerLeuAenSerArgValThrMet 69
    |||||
Qy 61 GATATTAGC-----
    |||
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuArgLeuAenSerValThrAlaAlaAsp 89
    |||||
Qy 70 -----AGCTGG 75
    |||||
Db 90 ThrAlaValTyrTyrCysAlaArgValSerTrp 100
    |||||
RESULT 4
US-09-880-748-993
; Sequence 993, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-993
Alignment Scores:
Pred. No.: 0.00905 Length: 250
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 15 Gaps: 1
NOLAN463-1A.SEQ (1-81) x US-10-293-418-993 (1-250)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCTCAAGAGTCGGCG----- 54
    |||||
Db 50 GluileAenHisSerGlySerThrAsnTyrAsnProSerLeuAenSerArgValThrIle 69
    |||||
Qy 55 AGTCAGGATATTAGCAGC 72
    |||||
Db 70 SerGlnAspThrSerAsn 75
    |||||
RESULT 5
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954
Alignment Scores:
Pred. No.: 0.00908 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
```

```
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-993
Alignment Scores:
Pred. No.: 0.00905 Length: 250
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 15 Gaps: 1
NOLAN463-1A.SEQ (1-81) x US-10-293-418-993 (1-250)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCTCAAGAGTCGGCG----- 54
    |||||
Db 50 GluileAenHisSerGlySerThrAsnTyrAsnProSerLeuAenSerArgValThrIle 69
    |||||
Qy 55 AGTCAGGATATTAGCAGC 72
    |||||
Db 70 SerGlnAspThrSerAsn 75
    |||||
RESULT 6
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954
Alignment Scores:
Pred. No.: 0.00908 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
```

```
DB: 10 Gaps: 1
NOLAN463-1A.SEQ (1-81) x US-09-880-748-954 (1-253)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGGCG----- 54
Db 50 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuAsnSerArgValThrIle 69
Qy 55 AGTCAGGATATTACAGC 72
Db 70 SerGlnAspThrSerAsn 75
RESULT 7
US-10-293-418-954
; Sequence 954, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-954
Alignment Scores:
Pred. No.: 0.00908 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 15 Gaps: 1
NOLAN463-1A.SEQ (1-81) x US-10-293-418-954 (1-253)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGGCG----- 54
Db 50 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuAsnSerArgValThrIle 69
Qy 55 AGTCAGGATATTACAGC 72
Db 70 SerGlnAspThrSerAsn 75
RESULT 8
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
```

```
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2
Alignment Scores:
Pred. No.: 0.0107 Length: 80
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 14 Gaps: 0
NOLAN463-1A.SEQ (1-81) x US-10-078-958-2 (1-80)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
Db 33 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuAsnSerArgValThr--- 51
Qy 61 GATATTAGC 69
Db 52 ---IleSer 53
RESULT 9
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40
Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 14 Gaps: 0
NOLAN463-1A.SEQ (1-81) x US-10-194-975-40 (1-97)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGGCGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyAsnProSerLeuAsnSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70
RESULT 10
```

US-10-308-817-83
; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-308-817-83 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---lleser 70

RESULT 11
US-10-032-037B-87
; Sequence 87, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-032-037B-87 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---lleser 70

Db 69 ---lleser 70

RESULT 12
US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-029-988B-87 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---lleser 70

RESULT 13
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-032-423A-87 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60

Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 14
US-10-453-698-83
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-453-698-83 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 15
US-10-029-926B-87
; Sequence 87, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.: 0.0112 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

NOLAN463-1A.SEQ (1-81) x US-10-029-926B-87 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

Search completed: August 4, 2005, 18:49:48
Job time : 87.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:04:24 ; Search time 18.25 Seconds
(without alignments)
854.089 Million cell updates/sec

Title: NOLAN463-1A.SEQ

Perfect score: 140

Sequence: 1 GAATCATCATAGTGAAG.....ATATTAGCAGCTGGTTAGCC 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cg2 1/USPTO.spool_P/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5
-DB=PIR -OPMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN08728463-1 @CGN 1 1 77 @runat_04082005_125806_24544 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -YGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 94 | 67.1 | 97 | 2 | S26806 |
| 2 | 93.9 | 67.1 | 140 | 2 | S78052 |
| 3 | 92.4 | 66.0 | 97 | 2 | S26898 |
| 4 | 92.4 | 66.0 | 97 | 2 | S26805 |
| 5 | 92.4 | 66.0 | 106 | 2 | S37454 |
| 6 | 92.4 | 66.0 | 122 | 2 | JL0047 |
| 7 | 92.4 | 66.0 | 126 | 2 | S47010 |
| 8 | 92.4 | 66.0 | 133 | 2 | F50341 |
| 9 | 92.4 | 66.0 | 140 | 2 | A49028 |
| 10 | 92.4 | 66.0 | 143 | 2 | B49028 |
| 11 | 92.4 | 66.0 | 231 | 2 | B23746 |
| 12 | 88.4 | 63.1 | 97 | 2 | G34964 |
| 13 | 84.4 | 60.3 | 98 | 2 | S26905 |
| 14 | 83.4 | 59.6 | 97 | 2 | S14474 |

| | | | | | | |
|----|------|------|-----|---|--------|---------------------|
| 15 | 81.4 | 58.1 | 129 | 2 | S44114 | Ig heavy chain V r |
| 16 | 80.4 | 57.4 | 134 | 2 | S54906 | Ig heavy chain V r |
| 17 | 80 | 57.1 | 123 | 2 | S30529 | Ig heavy chain V r |
| 18 | 79.1 | 56.5 | 140 | 2 | I37782 | Ig variable region |
| 19 | 78.4 | 56.0 | 98 | 2 | S26904 | Ig heavy chain V r |
| 20 | 78.4 | 56.0 | 145 | 2 | S78055 | Ig heavy chain pre |
| 21 | 78.4 | 56.0 | 146 | 1 | G1HUH2 | Ig heavy chain pre |
| 22 | 77.4 | 55.3 | 114 | 2 | I72667 | cold agglutinin FS |
| 23 | 77.3 | 55.2 | 130 | 2 | S31673 | Ig heavy chain V r |
| 24 | 77 | 55.0 | 134 | 2 | B24672 | Ig heavy chain pre |
| 25 | 75.4 | 53.9 | 97 | 2 | JH0428 | Ig gamma chain V r |
| 26 | 74.4 | 53.1 | 106 | 2 | S26464 | Ig heavy chain V r |
| 27 | 74 | 52.9 | 116 | 2 | S38718 | Ig heavy chain V r |
| 28 | 73.4 | 52.4 | 97 | 2 | S26906 | Ig heavy chain V r |
| 29 | 73.4 | 52.4 | 97 | 2 | S12416 | Ig heavy chain V r |
| 30 | 73.4 | 52.4 | 99 | 2 | S12412 | Ig heavy chain V r |
| 31 | 73.4 | 52.4 | 105 | 2 | S44125 | Ig lambda chain V r |
| 32 | 73.4 | 52.4 | 116 | 2 | B26340 | Ig heavy chain pre |
| 33 | 73.4 | 52.4 | 118 | 2 | A26340 | Ig heavy chain pre |
| 34 | 73.4 | 52.4 | 130 | 2 | S31690 | Ig heavy chain V r |
| 35 | 73.1 | 52.2 | 127 | 2 | S19668 | Ig heavy chain V r |
| 36 | 72 | 51.4 | 97 | 2 | S26804 | Ig heavy chain V r |
| 37 | 72 | 51.4 | 97 | 2 | S26808 | Ig heavy chain V r |
| 38 | 72 | 51.4 | 116 | 2 | S18557 | Ig heavy chain V r |
| 39 | 72 | 51.4 | 137 | 2 | S31676 | Ig heavy chain V r |
| 40 | 72 | 51.4 | 139 | 2 | S31696 | Ig heavy chain V r |
| 41 | 72 | 51.4 | 139 | 2 | S31586 | Ig heavy chain V r |
| 42 | 71.5 | 51.1 | 109 | 2 | PH1673 | Ig heavy chain V r |
| 43 | 71.4 | 51.0 | 97 | 2 | PL0118 | Ig heavy chain V-I |
| 44 | 71.4 | 51.0 | 98 | 2 | S26902 | Ig heavy chain V r |
| 45 | 71.4 | 51.0 | 98 | 2 | S12421 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

S26806

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26806

R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Eur. J. Immunol. 22, 1075-1082, 1992

A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A/Reference number: S26800; MUID:92201299; PMID:1348029

A/Accession: S26806

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-97 <WEN>

A/Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

| | | | |
|------------------------|----------|---------------|----|
| Pred. No.: | 0.000964 | Length: | 97 |
| Score: | 94.00 | Matches: | 17 |
| Percent Similarity: | 83.33% | Conservative: | 3 |
| Best Local Similarity: | 70.83% | Mismatches: | 4 |
| Query Match: | 67.14% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

NOLAN463-1A.SEQ (1-81) x S26806 (1-97)

Qy 1 GAATCATCATAGTGAAGCACCACCTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60

Db 50 GUILLEASHHISSErGlySerThrAsnProSerLeuLysSerArgIleThrMet 69

Qy 61 GATATTAGCAGC 72

Db 70 SerValAspThr 73

RESULT 2

S78052

Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78052; S23717
R;Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X5441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.

A;Reference number: S23716; MUID:92031262; PMID:1718404

A;Accession: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X5441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 0.00102 | Length: | 140 |
| Score: | 93.90 | Matches: | 21 |
| Percent Similarity: | 33.85% | Conservative: | 1 |
| Best Local Similarity: | 32.31% | Mismatches: | 2 |
| Query Match: | 67.07% | Indels: | 41 |
| DB: | 2 | Gaps: | 1 |

NOLAN463-1A.SEQ (1-81) x S78052 (1-140)

| | | | |
|----|-----|--|-----|
| Qy | 1 | GAATCAATCATAGTGGAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG | 60 |
| Db | 64 | GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- | 82 |
| Qy | 61 | GATATTAGC----- | 69 |
| Db | 83 | ---IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAla | 101 |
| Qy | 70 | -----AGCTGG | 75 |
| Db | 102 | AlaAspThrAlaValTyrTyrCysAlaArgGlyGlySerValLeuArgPheLeuGluTrp | 121 |
| Qy | 76 | TTA 78 | |
| Db | 122 | Leu 122 | |

RESULT 3

S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898; S12420
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404389
A;Accession: S26898
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference number: S09421; MUID:90059975; PMID:2511001
A;Accession: S12420

A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-97 <SAN>
A;Cross-references: EMBL:X56364
A;Experimental source: V(H)4.2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

| | | | |
|------------------------|---------|---------------|----|
| Alignment Scores: | | Length: | 97 |
| Pred. No.: | 0.00156 | Matches: | 19 |
| Score: | 92.40 | Conservative: | 1 |
| Percent Similarity: | 74.07% | Mismatches: | 1 |
| Best Local Similarity: | 70.37% | Indels: | 6 |
| Query Match: | 66.00% | Gaps: | 0 |
| DB: | 2 | | |

NOLAN463-1A.SEQ (1-81) x S26898 (1-97)

| | | | |
|----|----|--|----|
| Qy | 1 | GAATCAATCATAGTGGAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG | 60 |
| Db | 50 | GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- | 68 |
| Qy | 61 | GATATTAGC | 69 |
| Db | 69 | ---IleSer | 70 |

RESULT 4

S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26805
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

| | | | |
|------------------------|---------|---------------|----|
| Alignment Scores: | | Length: | 97 |
| Pred. No.: | 0.00156 | Matches: | 19 |
| Score: | 92.40 | Conservative: | 1 |
| Percent Similarity: | 74.07% | Mismatches: | 1 |
| Best Local Similarity: | 70.37% | Indels: | 6 |
| Query Match: | 66.00% | Gaps: | 0 |
| DB: | 2 | | |

NOLAN463-1A.SEQ (1-81) x S26805 (1-97)

| | | | |
|----|----|--|----|
| Qy | 1 | GAATCAATCATAGTGGAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG | 60 |
| Db | 50 | GlulleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- | 68 |
| Qy | 61 | GATATTAGC | 69 |
| Db | 69 | ---IleSer | 70 |

RESULT 5

S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from

A:Reference number: S37453
A:Accession: S37454
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <MC1>
A:Cross-references: EMBL:X75022; NID:q404311; PIDN:CAAS2930.1; PID:g758093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Alignment Scores:
Pred. No.: 0.00157 Length: 106
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x S37454 (1-106)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 28 GlulleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLysSerArgValThr--- 46
:::

Qy 61 GATATTAGC 69
|||||
Db 47 ---IleSer 48

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
A:Accession: JL0047
R:Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5'
A:Reference number: JL0047; MUID:88258392; PMID:3133445
A:Accession: JL0047
A:Molecule type: mRNA
A:Residues: 1-122 <BAE>
A:Experimental source: T-cell line RPMI 8402
A:Note: the authors translated the reading frame which extends to the stop codon; the se
A:Note: this sequence belongs to the VH II subgroup
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00159 Length: 122
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x JL0047 (1-122)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 58 GlulleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLysSerArgValThr--- 76
:::

Qy 61 GATATTAGC 69
|||||
Db 77 ---IleSer 78

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
A:Accession: S47010
R:Mamoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994

A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A:Reference number: S47009
A:Accession: S47010
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z35492; NID:9517254; PIDN:CAA84625.1; PID:g517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00159 Length: 126
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x S47010 (1-126)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLysSerArgValThr--- 68
:::

Qy 61 GATATTAGC 69
|||||
Db 69 ---IleSer 70

RESULT 8
PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
A:Accession: PS0341
R:Ratech, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A:Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
A:Reference number: PS0341; MUID:92171937; PMID:1540170
A:Accession: PS0341
A:Molecule type: mRNA
A:Residues: 1-133 <RAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-38/Region: framework 1
F:39-43/Region: complementarity-determining 1
F:44-57/Region: framework 2
F:58-74/Region: complementarity-determining 2
F:75-106/Region: framework 3

Alignment Scores:
Pred. No.: 0.0016 Length: 133
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x PS0341 (1-133)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 58 GlulleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLysSerArgValThr--- 76
:::

Qy 61 GATATTAGC 69
|||||
Db 77 ---IleSer 78

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045; MUID:92324290; PMID:1623923

C;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <RI>
A;Cross-references: GB:S39381; NID:G250899; PIDN:AAB2441.1; PID:G250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00161 Length: 140
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x A49045 (1-140)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 69 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 87
:::

Qy 61 GATATTAGC 69
Db 88 ---IleSer 89
|||||

RESULT 10

B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549

C;Accession: B49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TIM>
A;Cross-references: GB:S64473; NID:G236906; PIDN:AAB20012.1; PID:G236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00161 Length: 143
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x B49028 (1-143)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
:::

Qy 61 GATATTAGC 69
Db 69 ---IleSer 70
|||||

RESULT 11

Ig heavy chain V region (DP-70 / 4.19) - human (fragment)

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660

A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00167 Length: 231
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x B23746 (1-231)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 49 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 67
:::

Qy 61 GATATTAGC 69
Db 68 ---IleSer 69
|||||

RESULT 12

G34964
Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188

A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00524 Length: 97
Score: 88.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 63.14% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x G34964 (1-97)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCCCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlyThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
:::

Qy 61 GATATTAGC 69
Db 69 ---IleSer 70
|||||

RESULT 13

S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26905; S12419
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference numbers: S26885; MUID:93021117; PMID:1404388
A;Accession: S26905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A;Note: designated DP-70
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A;Title: The smaller human V(H) gene families display remarkably little polymorphism.
A;Reference numbers: S09421; MUID:90059975; PMID:2511001
A;Accession: S12419
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <SAN>
A;Cross-references: EMBL:X56363
A;Note: designated 4.19
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.0176 Length: 98
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x S26905 (1-98)

Qy 1 GAAATCAATCATAGTGAAGCACCACCTACAAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db 51 GlulileTyHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 69
Qy 61 GATATTAGC 69
Db 70 ---IleSer 71

RESULT 14
S14474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H.
submitted to the EMBL Data Library, November 1990
A;Reference numbers: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESJ>
A;Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:gl335354
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.0238 Length: 97
Score: 83.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 59.57% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x S14474 (1-97)

C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable x
A;Reference numbers: S44105
A;Accession: S44114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HAW>
A;Cross-references: EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.0444 Length: 129
Score: 81.40 Matches: 17
Percent Similarity: 67.86% Conservative: 2
Best Local Similarity: 60.71% Mismatches: 3
Query Match: 58.14% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x S44114 (1-129)

Qy 1 GAAATCAATCATAGTGAAGCACCACCTACAAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
Db 51 GlulileTyHisSerGlySerThrAsnTyAsnProSerPheLysSerArgValThr--- 69
Qy 61 GATATTAGC 72
Db 70 ---IleSerAla 72

Search completed: August 4, 2005, 18:21:23
Job time : 20.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 17:55:57 ; Search time 83.75 Seconds
(without alignments)
990.529 Million cell updates/sec

Title: NOLAN463-1A.SEQ

Perfect score: 140

Sequence: 1 GAAATCAATCATAGTGAAG.....ATATTAGCAGCTGGTTAGCC 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Zgapop 6.0 , Zgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2/1/USPTO.spool_p/NOLAN08728463-1/runat_04082005_125806_24533/app_query.fasta_1.5
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1@cgn.1.1.305 @runat_04082005_125806_24533 -NCPU=6
-ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : UniProt 03:*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------|--------------------|
| 1 | 92.4 | 66.0 | 116 | Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 2 | 92.4 | 66.0 | 595 | Q8WUX4 | Q8WUX4 homo sapien |
| 3 | 92.4 | 66.0 | 597 | Q6GMX5 | Q6GMX5 homo sapien |
| 4 | 92.4 | 66.0 | 597 | Q9BU10 | Q9BU10 homo sapien |
| 5 | 92.4 | 66.0 | 625 | Q96AA6 | Q96AA6 homo sapien |
| 6 | 86.4 | 61.7 | 597 | Q9B0B8 | Q9B0B8 homo sapien |
| 7 | 84.4 | 60.3 | 576 | Q6P4I8 | Q6P4I8 homo sapien |
| 8 | 81.3 | 58.1 | 477 | Q6GMX7 | Q6GMX7 homo sapien |
| 9 | 78.4 | 56.0 | 146 | 1 | Q7Z3Y6 |
| 10 | 73.7 | 52.6 | 139 | 1 | HV21 HUMAN |
| 11 | 72.6 | 51.9 | 479 | 2 | Q86SX2 |
| 12 | 72 | 51.4 | 465 | 2 | Q99M22 |
| 13 | 72 | 51.4 | 620 | 2 | Q6GMX6 |
| 14 | 70.6 | 50.4 | 262 | 2 | Q96EY0 |
| 15 | 69.3 | 49.5 | 119 | 2 | Q65Z11 |
| 16 | 69.1 | 49.4 | 113 | 1 | Q9UL73 |
| | | | | | HV47_MOUSE |

| | | | | | |
|----|------|------|------|---|------------|
| 17 | 69 | 49.3 | 116 | 1 | HV61_MOUSE |
| 18 | 67.4 | 48.1 | 2348 | 2 | Q8Z027 |
| 19 | 66.9 | 47.8 | 476 | 2 | Q6GMX1 |
| 20 | 65 | 46.4 | 116 | 1 | HV60_MOUSE |
| 21 | 65 | 46.4 | 478 | 2 | Q6NVH3 |
| 22 | 64 | 45.7 | 478 | 2 | Q7Z379 |
| 23 | 60.8 | 43.4 | 3118 | 2 | Q17575 |
| 24 | 59.5 | 42.5 | 1160 | 1 | TFC3_YEAST |
| 25 | 59.4 | 42.4 | 150 | 2 | Q95973 |
| 26 | 59.1 | 39.7 | 274 | 2 | Q9FL48 |
| c | 59 | 42.1 | 136 | 2 | Q6LB05 |
| 27 | 59 | 42.1 | 137 | 1 | HV45_MOUSE |
| 28 | 59 | 42.1 | 209 | 1 | UPP_OCEIH |
| 29 | 58.7 | 41.9 | 209 | 2 | Q8XWU0 |
| c | 58.6 | 39.3 | 451 | 2 | Q6NGD8 |
| 30 | 58.6 | 39.3 | 467 | 1 | DPO4_CORGL |
| c | 57.8 | 41.3 | 1083 | 1 | KG88_HUMAN |
| 32 | 57.5 | 41.1 | 393 | 2 | Q7WZ77 |
| 34 | 57.5 | 41.1 | 963 | 2 | Q8P5M2 |
| 35 | 57.4 | 41.0 | 496 | 2 | Q96KX8 |
| 36 | 57.2 | 40.9 | 729 | 1 | DCMA_MOOTH |
| c | 57 | 38.3 | 337 | 2 | Q6LOH3 |
| 38 | 57 | 40.7 | 1916 | 2 | Q9VKG8 |
| 39 | 56.7 | 40.5 | 212 | 2 | Q926K5 |
| 40 | 56.6 | 40.4 | 360 | 2 | Q92UL5 |
| 41 | 56.6 | 40.4 | 408 | 1 | YBX0_ARATH |
| 42 | 56.4 | 40.3 | 390 | 2 | Q6HH60 |
| 43 | 56.4 | 40.3 | 545 | 2 | Q6HH58 |
| 44 | 56.4 | 40.3 | 588 | 2 | Q813F9 |
| 45 | | | | | |

ALIGNMENTS

RESULT 1
Q7Z3Y6 PRELIMINARY; PRT; 116 AA.
ID Q7Z3Y6
AC Q7Z3Y6; (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN Names:VH4-34;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauning A.,
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -
DR HSSP; P18532; IKCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12902 MW; CE3D8A84616C908 CRC64;

Alignment Scores:
Pred. No.: 0.00339 Length: 116
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x Q7Z3Y6 (1-116)

QY 1 GAAATCAATCATAGTGAAGCACCACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60

| | | |
|---|---|---|
| QY | 61 | GATATTACG 69 |
| DB | 95 | ---lleSer 96 |
| RESULT 3 | | |
| ID | Q6GMX5 | PRELIMINARY; PRT; 597 AA. |
| QC | Q6GMX5; | |
| AC | 05-JUL-2004 | (TREMBLrel. 27, Created) |
| DC | 05-JUL-2004 | (TREMBLrel. 27, Last sequence update) |
| DT | 05-JUL-2004 | (TREMBLrel. 27, Last annotation update) |
| DE | Hypothetical protein. | |
| OC | Homo sapiens (Human). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| OX | NCBI_TaxID=9606; | |
| RN | [1] | |
| RC | SEQUENCE FROM N.A. | |
| RC | TISSUE=Lymph; | |
| RC | MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | |
| RA | Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | |
| RA | Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., | |
| RA | Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | |
| RA | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | |
| RA | Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | |
| RA | Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S., | |
| RA | Krzyszynski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., | |
| RA | Jones S.J., Marra M.A.; | |
| RT | "Generation and initial analysis of more than 15,000 full-length human | |
| RT | and mouse cDNA sequences." | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | |
| RL | [2] | |
| RC | SEQUENCE FROM N.A. | |
| RC | TISSUE=Lymph; | |
| RL | Strausberg R.; | |
| RL | Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; BC073767; AAH73767.1; -. | |
| DR | InterPro; IPR003599; IG. | |
| DR | InterPro; IPR007110; IG-like. | |
| DR | InterPro; IPR003597; IG c1. | |
| DR | InterPro; IPR003006; IG MHC. | |
| DR | InterPro; IPR003596; IG v. | |
| DR | Pfam; PF07654; Cl-set; 4. | |
| DR | Pfam; PF00047; IG; 4. | |
| DR | SMART; SM00409; IG; 2. | |
| DR | SMART; SM00407; IGc1; 4. | |
| DR | SMART; SM00406; IGv; 1. | |
| DR | PROSITE; PS50835; IG LIKE; 5. | |
| DR | PROSITE; PS00290; IG MHC; UNKNOWN_3. | |
| KW | Hypothetical protein. | |
| SC | SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64; | |
| Alignment Scores: | | |
| Pred. No.: | 0.00427 | Length: 597 |
| Score: | 92.40 | Matches: 19 |
| Percent Similarity: | 74.07% | Conservative: 1 |
| Best Local Similarity: | 70.37% | Mismatches: 1 |
| Query Match: | 66.00% | Indels: 6 |
| DB: | 2 | Gaps: 0 |
| NOLAN463-1A_SEQ (1-81) x Q6GMX5 (1-597) | | |

```
Db 69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
|||
Qy 61 GATATTAGC 69
|||
Db 88 ---IleSer 89
|||

RESULT 4
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Halse S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the ENBL/GenBank/DBBJ databases.
DR EMBL; BC002963; AAH02963.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.: 0.00427 Length: 597
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x Q9BU10 (1-597)
```

```
Qy 1 GAAATCAATCATAGTGGAGACCACTACAAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
|||
```

```
Qy 61 GATATTAGC 69
|||
Db 88 ---IleSer 89
|||

RESULT 5
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Halse S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the ENBL/GenBank/DBBJ databases.
DR EMBL; BC017356; AAH17356.2; -
DR PIR; S15590; S15590.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.: 0.00429 Length: 625
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x Q96AA6 (1-625)
```

```
Qy 1 GAAATCAATCATAGTGGAGACCACTACAAACCCGTCCTCAAGAGTCGGCGAGTCAG 60
```

```
Db 76 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 94
Qy 61 GATATTAGC 69
Db 95 ---IleSer 96

RESULT 6
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR HSP; P01861; IADO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.: 0.0281 Length: 597
Score: 86.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 61.71% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x Q9BQB8 (1-597)

Qy 1 GAAATCAATCATAGTGAAGCACCACCTACACCCCTCAAGAGTCGGCGAGTCAG 60
Db 69 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
```

```
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 7
Q6P4I8 PRELIMINARY; PRT; 576 AA.
AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSP; P01820; IA7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00047; Iq; 1.
DR SMART; SM00409; Iq; 1.
DR SMART; SM00407; Iqcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 0.0524 Length: 576
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 2 Gaps: 0

NOLAN463-1A.SEQ (1-81) x Q6P4I8 (1-576)
```

QY 1 GAATCAATCATAGTGAAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
 Db 77 GluileuHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 95
 QY 61 GATATTAGC 69
 Db 96 ---IleSer 97

RESULT 8
 Q6GMX7
 ID Q6GMX7 PRELIMINARY; PRT; 477 AA.
 AC O6GMX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073765; AAH73765.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Alignment Scores:
 Pred. No.: 0.135 Length: 477
 Score: 81.30 Matches: 17
 Percent Similarity: 39.22% Conservative: 3
 Best Local Similarity: 33.33% Mismatches: 4
 Query Match: 58.07% Indels: 27
 DB: 2 Gaps: 1

QY 1 GAATCAATCATAGTGAAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
 Db 77 GluileuHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 95
 QY 61 GATATTAGC 69
 Db 96 ---IleSer 97

RESULT 10
 Q86SX2

NOLAN463-1A.SEQ (1-81) x Q6GMX7 (1-477)
 QY 4 ATCAATCATAGTGAAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAGGAT 63
 Db 70 IleSerHisSerGlySerThrThrTyrAsnProSerLeuLysSerArgValThrLeuSer 89
 QY 64 ATT----- 66
 Db 90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
 QY 67 -----AGCAGCTGG 75
 Db 110 AlaValTyrTyrCysAlaHisGlySerSerTyr 120

RESULT 9
 HV2I_HUMAN
 ID HV2I_HUMAN STANDARD; PRT; 146 AA.
 AC P06331;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
 repeat sequence in 5' flanking region.";
 RL Gene 33:181-189 (1985).
 DR PIR; A02101; GIHUH2.
 DR HSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 RN SIGNAL 1 19
 FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
 FT DOMAIN 20 117 V segment.
 FT DOMAIN 118 127 D segment.
 FT DOMAIN 128 146 J segment.
 FT DISULFID 42 115 By similarity.
 FT NON TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 8D7PD52BB218171F CRC64;

Alignment Scores:
 Pred. No.: 0.285 Length: 146
 Score: 78.40 Matches: 17
 Percent Similarity: 66.67% Conservative: 1
 Best Local Similarity: 62.96% Mismatches: 3
 Query Match: 56.00% Indels: 6
 DB: 1 Gaps: 0

NOLAN463-1A.SEQ (1-81) x HV2I_HUMAN (1-146)
 QY 1 GAATCAATCATAGTGAAGACCACTACACCCGTCCTCAAGAGTCGGCGAGTCAG 60
 Db 70 GluileuHisSerGlySerThrAsnTyrLysThrSerLeuLysSerArgValThr--- 88
 QY 61 GATATTAGC 69
 Db 89 ---IleSer 90

RESULT 10
 Q86SX2

ID Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSDDL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAB62627.1; -;
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
Alignment Scores:
Pred. No.: 1.24 Length: 139
Score: 73.70 Matches: 17
Percent Similarity: 35.71% Conservative: 3
Best Local Similarity: 30.36% Mismatches: 33
Query Match: 52.64% Indels: 33
DB: 2 Gaps: 1
NOLAN463-1A.SEQ (1-81) x Q86SX2 (1-139)
QY 4 ATCAATCATAGTGAAGACCAACTACACCGCTCCCTCAAGAGTCGGCGAGT----- 57
Db 83 ILEtyrtyrSerGlySerThrAsnTyAsnProSerSerLeuLysSerArgValThrIleSer 102
QY 57 ----- 57
Db 103 ValAspThrSerLysAsnGlnPheSerLeuLysSerSerValThrAlaAlaAspThr 122
QY 58 -----CAGGATATTAGCAGC 72
Db 123 AlaValtyrtyrCysAlaArgAspThrValArgGlyAspValSerSer 138
RESULT 11
Q99M22
ID Q99M22 PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Carnison R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AA02091.1; -;
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
Alignment Scores:
Pred. No.: 2.08 Length: 479
Score: 72.60 Matches: 17
Percent Similarity: 33.93% Conservative: 2
Best Local Similarity: 30.36% Mismatches: 4
Query Match: 51.86% Indels: 34
DB: 2 Gaps: 1
NOLAN463-1A.SEQ (1-81) x Q99M22 (1-479)
QY 4 ATCAATCATAGTGAAGACCAACTACACCGCTCCCTCAAGAGTCGGCGAGTCA--- 59
Db 70 ILEAsnTyAspGlySerAsnAsnTyAsnProSerSerLeuLysAsnArgIleSerIleThr 89
QY 59 ----- 59
Db 90 ArgAspThrSerLysAsnGlnPhePheLeuLysLeuAsnSerValThrThrGluAspThr 109
QY 60 -----GGATATTAGCAGCTGG 75
Db 110 AlaThrtyrtyrCysAlaSerArgGlytyr-----SerTrp 121
RESULT 12
Q6GMX6
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;

RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073766; AAH73766.1; -;
 DR InterPro: IPR003599; Ig-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig cl.
 DR InterPro: IPR003006; Ig MHC.
 DR InterPro: IPR003596; Ig v.
 DR Pfam: PF07654; Cl-set; 3.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.

SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores: 2.5 Length: 465
 Pred. No.: 72.00 Matches: 13
 Score: 80.00% Conservations: 3
 Percent Similarity: 80.00% Mismatches: 4
 Best Local Similarity: 65.00% Indels: 0
 Query Match: 51.43% Gaps: 0
 DB: 2

NOLAN463-1A.SEQ (1-81) x Q6GMX6 (1-465)

QY 13 AGTGAAGACCAACTACACCGCTCCCTCAAGAGTCGGCGAGTCAGGATATTAGCAGC 72
 |||||
 Db 73 SerGlySerThrAsnProSerLeuLysSerArgValThrMetSerValAspThr 92
 |||||

RESULT 13

Q96EYO PRELIMINARY; PRT; 620 AA.
 AC Q96EYO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;

RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011857; AAH11857.2; -;
 DR PIR: S15590; S15590.
 DR HSP: P01820; IG7J
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig cl.
 DR InterPro: IPR003006; Ig MHC.
 DR InterPro: IPR003596; Ig v.
 DR Pfam: PF07654; Cl-set; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.

SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Alignment Scores: 2.61 Length: 620
 Pred. No.: 72.00 Matches: 13
 Score: 80.00% Conservations: 3
 Percent Similarity: 80.00% Mismatches: 4
 Best Local Similarity: 65.00% Indels: 0
 Query Match: 51.43% Gaps: 0
 DB: 2

NOLAN463-1A.SEQ (1-81) x Q96EYO (1-620)

QY 13 AGTGAAGACCAACTACACCGCTCCCTCAAGAGTCGGCGAGTCAGGATATTAGCAGC 72
 |||||
 Db 80 SerGlySerThrAsnProSerLeuLysSerArgValThrMetSerValAspThr 99
 |||||

RESULT 14

Q65Z11 PRELIMINARY; PRT; 262 AA.
 AC Q65Z11;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Anti-HIV-1 reverse transcriptase single-chain variable.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hybridoma;
 RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
 RA MEDLINE=96211469; PubMed=8648670;
 RT "Targeting human immunodeficiency virus type 1 reverse transcriptase
 RT by intracellular expression of single-chain variable fragments to
 RT inhibit early stages of the viral life cycle.";
 RL J. Virol. 70:3392-3400 (1996).
 DR EMBL: U48716; AAB64342.1; -;

DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

DR InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00408; IGC2; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS50835; IG LIKE; 2.

KW RNA-directed DNA polymerase.

SQ SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 3.59 | Length: | 262 |
| Score: | 70.60 | Matches: | 16 |
| Percent Similarity: | 68.00% | Conservative: | 1 |
| Best Local Similarity: | 64.00% | Mismatches: | 4 |
| Query Match: | 50.43% | Indels: | 4 |
| DB: | 2 | Gaps: | 0 |

NOLAN463-1A.SEQ (1-81) x Q65211 (1-262)

Qy 4 ATCAATCATAGTGAAGCACCAACTACAAACCGTCCTCAAGAGTCGGCGAGTCAGGAT 63

Db 198 IleasTySerGlyAspThrTyTyrAsnProSerLeuLysSerArgIleSer----II 216

Qy 64 ATTAGCA 70

Db 216 eThrAla 218

RESULT 15

Q9UL73

ID Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR EMBL; AF035041; AAD56277.1; -.

DR PIR; PH0876; PH0876.

DR PIR; S12416; S12416.

DR HSP; P01820; IG7J.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; IG_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON TER 1

FT NON TER 119 119

SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 4.84 | Length: | 119 |
| Score: | 69.30 | Matches: | 15 |
| Percent Similarity: | 37.25% | Conservative: | 4 |
| Best Local Similarity: | 29.41% | Mismatches: | 5 |
| Query Match: | 49.50% | Indels: | 27 |
| DB: | 2 | Gaps: | 1 |

• NOLAN463-1A.SEQ (1-81) x Q9UL73 (1-119)

| | | | |
|----|----|--|-----|
| Qy | 4 | ATCAATCATAGTGAAGCACCAACTACAAACCGTCCTCAAGAGTCGGCGAGTCAGGAT | 63 |
| Db | 51 | IleTyTySerGlySerThrAsnTyThrProSerLeuLysSerArgValThrIleSer | 70 |
| Qy | 64 | ATT----- | 66 |
| Db | 71 | ValAspArgSerLysAsnGlnPheSerLeuLysLeuThrSerLeuThrAlaAlaAspThr | 90 |
| Qy | 67 | -----ACAGCTGG | 75 |
| Db | 91 | AlaValTyPheCysAlaArgLeuSerAsnTrp | 101 |

Search completed: August 4, 2005, 18:20:06

Job time : 89.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 17:55:32 ; Search time 92.5 Seconds
(without alignments)
677.353 Million cell updates/sec

Title: NOLAN463-1B.SEQ

Perfect score: 140

Sequence: 1 CGGCGAGTCTAGGATATTAG.....ACRACCCGTCCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/NOLAN08728463-1/runat_04082005_125805_24527/app.query.fasta_1.5
-DB-A Geneseq -QFMT=fastan -SUPFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USR=NOLAN08728463-1 @CGN 1.1 308 @runat_04082005_125805_24527 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=5
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

- 1: Geneseq16Dec04:*
- 2: Geneseq1980s:*
- 3: Geneseq1990s:*
- 4: Geneseq2000s:*
- 5: Geneseq2001s:*
- 6: Geneseq2002s:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 100.1 | 71.5 | 253 | 5 | Adp45322 Human Bly |
| 2 | 100.1 | 71.5 | 253 | 7 | Adg96149 Single ch |
| 3 | 99.9 | 71.4 | 125 | 6 | Ada89274 Human ant |
| 4 | 98.2 | 70.1 | 80 | 2 | Aaw62794 Amino aci |
| 5 | 98.2 | 70.1 | 97 | 2 | Aay05694 Multiple |
| 6 | 98.2 | 70.1 | 97 | 5 | Abg78212 Human Fv |
| 7 | 98.2 | 70.1 | 97 | 5 | Abg91903 Human ant |
| 8 | 98.2 | 70.1 | 97 | 6 | Abc27107 Human ger |
| 9 | 98.2 | 70.1 | 97 | 7 | Adb75646 Human pro |
| 10 | 98.2 | 70.1 | 97 | 7 | Add28104 Lymphoma |

| | | | | | |
|----|------|------|-----|---|--------------------|
| 11 | 98.2 | 70.1 | 97 | 7 | Adf10048 |
| 12 | 98.2 | 70.1 | 97 | 7 | Adf10150 |
| 13 | 98.2 | 70.1 | 97 | 7 | Adf09942 |
| 14 | 98.2 | 70.1 | 97 | 7 | Adj80323 VH gene 1 |
| 15 | 98.2 | 70.1 | 114 | 3 | Ab01949 |
| 16 | 98.2 | 70.1 | 114 | 3 | Ab01950 |
| 17 | 98.2 | 70.1 | 114 | 3 | Ab01953 |
| 18 | 98.2 | 70.1 | 114 | 3 | Ab01959 |
| 19 | 98.2 | 70.1 | 114 | 3 | Ab01952 |
| 20 | 98.2 | 70.1 | 114 | 3 | Ab01955 |
| 21 | 98.2 | 70.1 | 114 | 3 | Ab01956 |
| 22 | 98.2 | 70.1 | 114 | 3 | Ab01948 |
| 23 | 98.2 | 70.1 | 114 | 3 | Ab01954 |
| 24 | 98.2 | 70.1 | 114 | 7 | Adg70086 |
| 25 | 98.2 | 70.1 | 114 | 7 | Adg70013 |
| 26 | 98.2 | 70.1 | 116 | 2 | Aar66324 |
| 27 | 98.2 | 70.1 | 117 | 4 | Aam60904 |
| 28 | 98.2 | 70.1 | 117 | 4 | Abg55317 |
| 29 | 98.2 | 70.1 | 117 | 5 | Abg43454 |
| 30 | 98.2 | 70.1 | 118 | 6 | Ada89246 |
| 31 | 98.2 | 70.1 | 122 | 8 | Adk17418 |
| 32 | 98.2 | 70.1 | 122 | 8 | Adg42840 |
| 33 | 98.2 | 70.1 | 123 | 2 | Aaw03757 |
| 34 | 98.2 | 70.1 | 125 | 6 | Ada89266 |
| 35 | 98.2 | 70.1 | 139 | 3 | Aay99556 |
| 36 | 98.2 | 70.1 | 139 | 6 | Abw42859 |
| 37 | 98.2 | 70.1 | 139 | 7 | Abw02445 |
| 38 | 98.2 | 70.1 | 142 | 6 | Abp96287 |
| 39 | 98.2 | 70.1 | 154 | 6 | Abp96293 |
| 40 | 98.2 | 70.1 | 190 | 2 | Aay34304 |
| 41 | 98.2 | 70.1 | 202 | 2 | Aay34303 |
| 42 | 98.2 | 70.1 | 205 | 2 | Aay34299 |
| 43 | 98.2 | 70.1 | 218 | 7 | Adg70090 |
| 44 | 98.2 | 70.1 | 223 | 7 | Adj32112 |
| 45 | 98.2 | 70.1 | 224 | 7 | Adg70088 |

ALIGNMENTS

RESULT 1

ADP45322
ID ABP45322 standard; protein; 253 AA.

XX ABP45322;

AC AC

XX 19-AUG-2002 (first entry)

XX Human BlyS binding scFv SEQ ID 1333.

DE Human BlyS binding scFv SEQ ID 1333.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX OS

XX WO200202641-A1.

XX PD

XX 10-JAN-2002.

XX PF

XX 15-JUN-2001; 2001WO-US019110.

XX PR

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.
XX Synthetic.
OS Homo sapiens.
XX WO2003070752-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005128.
XX 20-FEB-2002; 2002US-0358994P.
XX (DYAX-) DYAX CORP.
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX Hoogenboom HRJM, Reiter Y;
XX WPI; 2003-663847/62.
XX N-PSDB; ADA89273.
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX Disclosure; Fig 28B; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC hTERT.

SQ Sequence 125 AA;

Alignment Scores:
Pred. No.: 0.000565 Length: 125
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 6 Gaps: 1

NOLAN463-1B.SEQ (1-81) x ADA89274 (1-125)

Qy 3 GGCGAGTCAGATATTAGCAGC-----
Db 26 GlyGlySer-----IleSerSerSerTyrTrpAlaTrpIleArgGlnProG1 44

Qy 25 -----TGTTAGCCGAAATCAATCATAGTGGAGGACCACTACACCCGTC 71
Db 44 YLysGlyLeuGluTrpIleGlyGluIleAsnHiserGlySerThrAsnTyAsnProse 64
Qy 72 CCTCAAGAGT 81
Db 64 rLeuLysSer 67
RESULT 4
AAW62794
ID AAW62794 standard; peptide; 80 AA.
XX AAW62794;
XX 23-SEP-1998 (first entry)
XX Amino acid sequence of a human antibody fragment.
XX Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX Homo sapiens.
OS
XX WO9824893-A2.
XX 11-JUN-1998.
XX 03-DEC-1997; 97WO-US023091.
XX 03-DEC-1996; 96US-00759620.
XX (ABGE-) ABGENIX INC.
XX Jakobovits A, Kucheralapati R, Klapholz S, Mendez M, Green L;
XX WPI; 1998-333314/29.
XX New transgenic non-human mammals - having an inactivated immunoglobulin
PT locus and a near complete human immunoglobulin locus, used for production
PT of human antibodies.
XX Disclosure; Page 71; 128pp; English.

XX AAW62793-822 represent fragments of human antibodies produced by
CC transgenic xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germline configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germline configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region. J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can be
CC used for the production of human antibodies when exposed to particular
CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX Sequence 80 AA;

Alignment Scores:
Pred. No.: 0.000842 Length: 80
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3

```
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x AAW62794 (1-80)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 25 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 42
Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 42 YrAsnProSerLeuLysSer 48

RESULT 5
AAY05694
ID AAY05694 standard; protein; 97 AA.
XX AC AAY05694;
XX DT 19-JUL-1999 (first entry)
XX DE Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
XX KW Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
XX KW heavy chain variable region; VH gene; somatic hypermutation;
XX KW B-cell clonality; RA gene; diagnosis; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Region 1..30
FT /label= FR1
FT Misc-difference 8 /note= "encoded by GGC"
FT Misc-difference 13 /note= "replaces Glu of RA"
FT Misc-difference 14 /note= "encoded by CCT"
FT Misc-difference 23 /note= "replaces Gly of RA"
FT Misc-difference 25 /note= "replaces Phe of RA"
FT Misc-difference 30 /note= "replaces Gly of RA"
FT Region 31..36
FT /label= CDR1
FT Misc-difference 31 /note= "replaces Gly of RA"
FT Misc-difference 32 /note= "replaces Phe of RA"
FT Region 37..50
FT /label= FR2
FT Region 51..66
FT /label= CDR2
FT Misc-difference 56 /note= "replaces Asn of RA"
FT Misc-difference 57 /note= "replaces Ser of RA"
FT Misc-difference 58 /note= "replaces Lys of RA"
FT Region 67..97
FT /label= FR3
FT Misc-difference 71 /note= "replaces Leu of RA"
FT Misc-difference 81 /note= "replaces Arg of RA"
XX WO9915696-A1.
XX 01-APR-1999.
XX 17-SEP-1998; 98WO-CA000873.
XX
```

```
PR 19-SEP-1997; 97CA-02216595.
PR 04-NOV-1997; 97CA-02220245.
XX
PA (QINY/) QIN Y.
XX QIN Y;
XX WPI; 1999-276985/23.
DR N-PSDB; AAX25318.
XX
XX Determination of B-cell clonality by amplification or enzymatic
XX digestion.
XX Disclosure; Fig 9D; 67pp; English.
XX
CC This sequence represents a heavy chain variable region (VH) as predicted
CC from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
CC fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
CC B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
CC in nucleotide and predicted amino acid (see AAY05691-94) sequences were
CC compared with the closest known germline VH genes; for 4d76, this was RA.
CC The results provided direct evidence that intrathecal clonally expanded B
CC -cells from the CSF of MS patients are hypermutated postgerminal centre
CC antibody-forming or memory lymphocytes that have undergone antigen
CC selection. This finding implicates an important pathogenic pathway for
CC the development of demyelination in CNS of MS. The invention provides
CC assay kits for determining B-cell or T-cell clonality. This technology
CC allows the establishment of clonal specific RNA library from pathogenic
CC cells in the CNS of patients, which is important for further
CC understanding of the role of antigen(s) in the cause of B-cell clonal
CC expansion, and towards developing antigen specific therapeutic strategy
XX
XX Sequence 97 AA;
SQ
```

```
Alignment Scores:
Pred. No.: 0.000883 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x AAY05694 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 59
Qy 62 ACAACCCGTCCTCAAGAGT 81
   |||
Db 59 YrAsnProSerLeuLysSer 65

RESULT 6
ABG78212
ID ABG78212 standard; protein; 97 AA.
XX AC ABG78212;
XX DT 15-NOV-2002 (first entry)
XX DE Human Fv molecule hypervariable region related peptide #87.
XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.
XX WO200259264-A2.
XX 01-AUG-2002.
XX 31-DEC-2001; 2001WO-US049440.
XX
```

XX 29-DEC-2000; 2000US-007511181.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 XX Plakain D, Peretz T;
 XX WPI; 2002-619166/66.
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 XX Claim 13; Page 193; 232pp; English.
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 97 AA;
 Alignment Scores:
 Pred. No.: 0.000883 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 5 Gaps: 0
 NOLAN463-1B-SEQ (1-81) x ABG78212 (1-97)
 Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACACT 61
 Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGTCCTCAAGAGT 81
 Db 59 yrAsnProSerLeuLysSer 65
 RESULT 7
 ABG91903
 ID ABG91903 standard; protein; 97 AA.
 XX AC ABG91903;
 XX
 XX 04-DEC-2002 (first entry)
 XX DE Human antibody fragment #87.
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX OS Homo sapiens.
 XX
 XX WO200253700-A2.
 XX

PD 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX Disclosure; Page 269; Opp; English.
 XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 XX Sequence 97 AA;
 Alignment Scores:
 Pred. No.: 0.000883 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 5 Gaps: 0
 NOLAN463-1B-SEQ (1-81) x ABG91903 (1-97)
 Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACACT 61
 Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGTCCTCAAGAGT 81
 Db 59 yrAsnProSerLeuLysSer 65
 RESULT 8
 ABG27107
 ID ABG27107 standard; protein; 97 AA.
 XX AC ABG27107;
 XX
 XX 10-SEP-2003 (first entry)
 XX DE Human germline heavy chain variable region gene segment #40.
 XX

XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human.

OS Homo sapiens.

PN WO2003074679

PD 12-SEP-2003.

03-MAR-2003; 2003WO-US006598.

PR 01-MAR-2002; 2002US-0360843P.

XX
XIT
COSTS
1960-7
20

PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.

Example 16; Fig 40a; 135pp; English.

The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody variable region sequence used to illustrate the invention.

| | | | |
|------------------------|---------|---------------|----|
| Sequence 97 AA; | | | |
| Alignment Scores: | | | |
| Pred. NO.: | 0.00083 | Length: | 97 |
| Score: | 98.20 | Matches: | 19 |
| Percent Similarity: | 65.62% | Conservative: | 2 |
| Best Local Similarity: | 59.38% | Mismatches: | 3 |
| Query Match: | 70.14% | Indels: | 8 |
| DB: | 7 | Gaps: | 0 |

NOLAN463-1B.SEO (1-81) x ADF10150 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAATAATCATAGTGGAGCACCAACT 61
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dh 42 GGVVVS---GVFVEN---GLUTRILEGVGLIIEANHSERGERLVSRTRASNT 59

62 ACAACCCGTCCTCAAGAGT 81

59 vrAsnProSerLeuLysSer 65

RESULT 13
ADF09942
ID ADF09942 standard; protein; 97 AA.

AC ADF09942;

DT 12-FEB-2004 (first entry)

DE Antibody heavy chain variable region VH 4-34.

KW Antibody; stability; solubility; antigen binding affinity;

KW variable region; human.

OS Homo sapiens.

PN WO2003074679-A2.

PD 12-SEP-2003.

03-MAR-2003; 2003WO-US006598.

PR 01-MAR-2002; 2002US-0360843P.

[illegible]XX
XX

XX
DR WPI; 2003-722066/68.

PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.

Disclosure; Fig 2a; 135pp; English.

The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody variable region sequence used to illustrate the invention.

[illegible]

NOLAN463-1B.SEO (1-81) x ADF09942 (1-97)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCAACCACT 61

pb 42 GlvIvs---GlvLeu---GluTrpIleGlvGluIleAsnH1sSerGlySerThrAsnT 59

62 ACAACCCGTCCCTCAAGAGT 81

pb 59 vrAsnProSerLeuLysSer 65

RESULT 14
ADJ80323
ID ADJ80323 standard; protein; 97 AA.

AC ADJ80323;

DT 06-MAY-2004 (first entry)

VH gene locus antibody amino acid sequence #43.

KW hybrid antibody; antibody; framework region; homology; immunogenicity.

OS Homo sapiens.

```

XX PN WO2003048321-A2.
XX PD 12-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038450.
XX PR 03-DEC-2001; 2001US-0336591P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Rother R, Wu D;
XX WPI; 2003-513753/48.
XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively
XX PT linking the selected framework sequences to one or more complementarity
XX PT determining regions of the initial antibody.
XX PS Disclosure; SEQ ID NO 83; 77pp; English.
XX CC The invention relates to a method of producing a hybrid antibody or
XX CC hybrid antibody fragment by: (i) providing an initial antibody having
XX CC specificity for a target; (ii) determining the sequence of a variable
XX CC region of the initial antibody; (iii) selecting a first component of the
XX CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
XX CC sequence of the first component to sequences contained in a reference
XX CC database of antibody sequences or antibody fragment sequences from a
XX CC target species; (v) selecting a sequence from an antibody in the database
XX CC which demonstrates a high degree of homology to the first component; (vi)
XX CC selecting a second component of the variable region which is different
XX CC than the first component, the second component selected from the group
XX CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
XX CC second component to sequences contained in a reference database of
XX CC antibody sequences or antibody fragment sequences from the target species
XX CC; (viii) selecting a sequence from the database which demonstrates a high
XX CC degree of homology to the second component and which is from a different
XX CC antibody than the selected antibody; and (ix) operatively linking the
XX CC selected framework sequences to one or more complementarity determining
XX CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
XX CC hybrid antibody fragment. The method is useful for producing a hybrid
XX CC antibody or hybrid antibody fragment (claimed). The antibody and
XX CC fragments are useful for therapeutic and diagnostic purposes. The method
XX CC uses entire framework regions from a single antibody variable heavy or
XX CC variable light chain to receive the CDRs. This produces antibodies that
XX CC are highly homologous and exhibit reduced immunogenicity while
XX CC maintaining an optimum binding profile. This sequence represents the
XX CC amino acid sequence of an antibody from the VH gene locus.
XX SQ Sequence 97 AA;

Alignment Scores:
Pred. No.: 0.000883 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 7 Gaps: 0

NOLAN463-1B.SEQ (1-81) x ADJ80323 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGACCAACT 61
Db 42 GlyLeu-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACACCCGTCCTCAAGAGT 81
Db 59 YrAsnProSerLeuLeuSer 65

RESULT 15
AAB01949
ID AAB01949 standard; protein; 114 AA.
XX

```

```

AC AAB01949;
XX 18-SEP-2000 (first entry)
XX DT
XX DE
XX KW Anti-Id1 Ab binding-defective mutant Ramos cell VH K70N/S77N.
XX KW Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
XX KW IgM; V gene diversity; directed constitutive hypermutation;
XX KW target sequence diversification; terminal deoxynucleotidyl transferase;
XX KW TdT; clonal expansion; selection; heavy chain variable region; VH;
XX KW mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 71
XX ET /note= "Encoded by CAG"
XX FN WO200022111-A1.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-GB003358.
XX PR 09-OCT-1998; 98GB-00022104.
XX PR 19-JAN-1999; 99GB-00001141.
XX PR 09-JUN-1999; 99GB-00013435.
XX PA (MED1-) MEDICAL RES COUNCIL.
XX PI Sale JE, Neuberger MS, Cumbers SJ;
XX WPI; 2000-317971/27.
XX N-PSDB; AA52435.
XX PT Lymphoid cell line preparation useful for producing gene products having
XX PT desired activity, involves screening and selecting cells having ongoing
XX PT target sequence diversification and higher mutation rates.
XX PS Example 5; Page; 69pp; English.
XX CC The invention relates to a method of preparing a lymphoid cell line
XX CC capable of capable of directed constitutive hypermutation of a target
XX CC nucleic acid region. The method comprises screening a cell population for
XX CC ongoing target sequence diversification and selecting a cell in which the
XX CC rate of target nucleic acid mutation exceeds that of other nucleic acid
XX CC mutation by a factor of 100 or more. The invention also relates to a
XX CC method for preparing a gene product with a desired activity, comprising
XX CC expressing a nucleic acid encoding the target gene operably linked to a
XX CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
XX CC transferase (Tdt), in the lymphoid cell line, and identifying a cell or
XX CC cells which express a mutated gene product with the desired activity. One
XX CC or more clonal populations of the identified cells is established, and
XX CC cells with an improved activity of interest are selected. These steps may
XX CC be iteratively repeated until a gene product with a desired activity
XX CC is obtained. The cell lines prepared according to the method of the
XX CC invention are used for directed constitutive hypermutation of a nucleic
XX CC acid region in the preparation of a gene product, preferably an enzyme or
XX CC an immunoglobulin (Ig) with a desired activity. In the exemplifications
XX CC of the invention, IgM-secreting Ramos cells were selected for use as they
XX CC undergo hypermutation during clonal expansion. This was determined on the
XX CC basis of the amount of diversity in the heavy chain variable region (VH).
XX CC Sequences AAB01949-B01954 represent various mutant Ramos cell IgM VHS
XX CC (AAB01949-B01954) which have lost the ability to bind anti-idiotypic
XX CC antibodies (anti-Id1 Ab) relative to the wild-type VH (AAB01948). Note:
XX CC The present sequence is not shown in the specification, but is derived
XX CC from the wild-type Ramos cell VH shown in figure 7
XX SQ Sequence 114 AA;

Alignment Scores:
Pred. No.: 0.00092 Length: 114

```

Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 3 Gaps: 0

NOLAN463-1B.SEQ (1-81) x AAB01949 (1-114)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGGAATCATCATAGTGGAGCACCACACT 61
 Db 36 GlyLys----GlyLeu----GlutrpIleGlyGlutIleAsnHisSerGlySerThrAsnT 53
 Qy 62 ACAACCGTCCTCAAGAGT 81
 Db 53 YrAsnProSerLeuLysSer 59

Search completed: August 4, 2005, 18:14:25
 Job time : 93.5 secs

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Alignment Scores:
Pred. No.: 0.00013 Length: 472
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 3 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-08-793-450-8 (1-472)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACACT 61
Db 61 Glylys---GlyLeu---GlutrpIleglyGluileAspHiserGlyserThrAsnt 78
QY 62 ACAACCCGTCCTCAAGAGT 81
Db 78 yrasnProSerLeuLysSer 84

RESULT 5

US-09-372-425A-6
Sequence 6, Application US/09372425A
Patent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
APPLICANT: Ramon Montano
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6
Alignment Scores:
Pred. No.: 0.000592 Length: 429
Score: 93.20 Matches: 18
Percent Similarity: 65.62% Conservative: 3
Best Local Similarity: 56.25% Mismatches: 3
Query Match: 66.57% Indels: 8
DB: 4 Gaps: 0
NOLAN463-1B.SEQ (1-81) x US-09-372-425A-6 (1-429)
QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAAGCACCACACT 61
Db 61 Glylys---GlyLeu---GlutrpIleglyGluileAspHiserGlyserThrAsnt 78
QY 62 ACAACCCGTCCTCAAGAGT 81
Db 78 yrasnProSerLeuLysSer 84
RESULT 6
US-09-025-769B-25
Sequence 25, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-025-769B-25

Alignment Scores:
Pred. No.: 0.000517 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-025-769B-25 (1-118)

QY 3 GCGAGTCAGATATTAGCAGC----- 24
   ||| ||| ||| ||| ||| |||
Db 26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGI 44
QY 25 -----TGCTTAGCCGAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAA 77
   |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
QY 78 GAGT 81
   ||| ||| |||
Db 64 sSer 65

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2020
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.: 0.000517 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-490-070A-25 (1-118)

QY 3 GCGAGTCAGATATTAGCAGC----- 24
   ||| ||| ||| ||| ||| |||
Db 26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysGI 44
QY 25 -----TGCTTAGCCGAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAA 77
   |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44 yLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
QY 78 GAGT 81
   ||| ||| |||
Db 64 sSer 65

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
```



```
Alignment Scores:
Pred. No.: 0.00071 Length: 120
Score: 91.10 Matches: 20
Percent Similarity: 52.27% Conservative: 3
Best Local Similarity: 45.45% Mismatches: 2
Query Match: 65.07% Indels: 19
DB: 3 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-08-545-809A-137 (1-120)
QY 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 45 GlyAspSer----IleSerSerGlyAsnTrpValArgGlnProProGlyLysG1 63
QY 25 -----TGCTTACCCGAATCATCATAGTGGAGCACCACACTAGAACCCGTCCTCAA 77
Db 63 yLeuGluTrpIleGlyGluIleHisHisSerGlySerThrTyrTyrAsnProSerLeu 83
QY 78 GAGT 81
Db 83 sSer 84

RESULT 11
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26...-1
US-09-471-276-835

Alignment Scores:
Pred. No.: 0.00257 Length: 147
Score: 87.20 Matches: 16
Percent Similarity: 65.62% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 62.29% Indels: 8
DB: 4 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-09-471-276-835 (1-147)
QY 2 GCGGAGTCAGGATATTAGCAGCTGGTTAGCCGNAATCAATCATAGTGGAGCAGCAACT 61
Db 69 GlyLys----GlyLeu----GluTrpIleSerGluIleAspHisGlyGlyAsnThrAsn 86
QY 62 ACAACCCGTCCTCAAGAGT 81
Db 86 yAsnProSerLeuLysSer 92

RESULT 12
US-08-466-151-5
; Sequence 5, Application US/08466151
```

```
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.: 0.00325 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 3 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-08-466-151-5 (1-130)
QY 1 CGGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
QY 22 -----AGCTGGTTAGCCGAAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
QY 40 AATCATAGTGAAGCACCACACTACACCCGTCCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 13
```

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.00325 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 3 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-08-466-163B-5 (1-130)

QY 1 CGGCGAGTCAGGATATTAG----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrThrLeuThrSerAsp 32
QY 22 -----AGCTGGTTAGCGGAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
QY 40 AATCATAGTCGAGCACCACCACTACAAACCGCTCCCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 14

US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-802-096-5

Alignment Scores:
Pred. No.: 0.00325 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 4 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-802-096-5 (1-130)

QY 1 CGGCGAGTCAGGATATTAG----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrThrLeuThrSerAsp 32
QY 22 -----AGCTGGTTAGCGGAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
QY 40 AATCATAGTCGAGCACCACCACTACAAACCGCTCCCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 15

US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.: 0.00325 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 4 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-802-077-5 (1-130)

QY 1 CGGCGAGTCAGGATATTAG----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrThrLeuThrSerAsp 32
QY 22 -----AGCTGGTTAGCGGAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
QY 40 AATCATAGTCGAGCACCACCACTACAAACCGCTCCCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

Search completed: August 4, 2005, 18:23:04
Job time : 24.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:20:25 ; Search time 80.25 Seconds
(without alignments)
788.093 Million cell updates/sec

Title: NOLAN463-1B.SEQ

Perfect score: 140

Sequence: 1 CGGCGGAGTCAGGATATTAG.....ACAACCCGTCCTCAAGAGT 81

Scoring table:

BLOSUM62
Q=cgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=cgapop 10.0, Xgapext 0.1
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blodum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000
-USER=NOLAN08728463-1 @CGN 1.1 260 @runat 04082005 125809 24629 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -RSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Published Applications AA:

1: /cgcn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgcn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
3: /cgcn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgcn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgcn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgcn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
7: /cgcn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgcn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgcn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgcn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgcn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgcn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgcn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgcn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgcn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgcn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
17: /cgcn2_6/ptodata/1/pubaa/US10E_PUBCOMB.pep.*
18: /cgcn2_6/ptodata/1/pubaa/US10F_NEW_PUB.pep.*
19: /cgcn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pep.*
20: /cgcn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
21: /cgcn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
22: /cgcn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 100.1 | 71.5 | 253 | 10 | US-09-880-748-1333 |
| 2 | 100.1 | 71.5 | 253 | 15 | US-10-293-418-1333 |
| 3 | 99.9 | 71.4 | 125 | 15 | US-10-371-942-118 |
| 4 | 98.2 | 70.1 | 80 | 14 | US-10-078-958-2 |
| 5 | 98.2 | 70.1 | 97 | 14 | US-10-194-975-40 |
| 6 | 98.2 | 70.1 | 97 | 15 | US-10-308-817-83 |
| 7 | 98.2 | 70.1 | 97 | 15 | US-10-032-037B-87 |
| 8 | 98.2 | 70.1 | 97 | 15 | US-10-029-988B-87 |
| 9 | 98.2 | 70.1 | 97 | 15 | US-10-032-423A-87 |
| 10 | 98.2 | 70.1 | 97 | 15 | US-10-453-698-83 |
| 11 | 98.2 | 70.1 | 97 | 15 | US-10-029-926B-87 |
| 12 | 98.2 | 70.1 | 97 | 16 | US-10-379-392-47 |
| 13 | 98.2 | 70.1 | 114 | 17 | US-10-733-532-128 |
| 14 | 98.2 | 70.1 | 115 | 17 | US-10-898-408-12 |
| 15 | 98.2 | 70.1 | 117 | 9 | US-09-864-761-44315 |
| 16 | 98.2 | 70.1 | 118 | 15 | US-10-371-942-90 |
| 17 | 98.2 | 70.1 | 118 | 17 | US-10-893-576-192 |
| 18 | 98.2 | 70.1 | 122 | 15 | US-10-360-828-63 |
| 19 | 98.2 | 70.1 | 125 | 15 | US-10-371-942-110 |
| 20 | 98.2 | 70.1 | 139 | 14 | US-10-300-675-2 |
| 21 | 98.2 | 70.1 | 139 | 17 | US-10-910-124-2 |
| 22 | 98.2 | 70.1 | 139 | 17 | US-10-893-576-43 |
| 23 | 98.2 | 70.1 | 142 | 17 | US-10-484-790A-10 |
| 24 | 98.2 | 70.1 | 223 | 10 | US-09-972-656-66 |
| 25 | 98.2 | 70.1 | 229 | 10 | US-09-972-656-82 |
| 26 | 98.2 | 70.1 | 230 | 10 | US-09-972-656-72 |
| 27 | 98.2 | 70.1 | 249 | 10 | US-09-880-748-1321 |
| 28 | 98.2 | 70.1 | 249 | 15 | US-10-293-418-1321 |
| 29 | 98.2 | 70.1 | 250 | 10 | US-09-880-748-1413 |
| 30 | 98.2 | 70.1 | 250 | 15 | US-10-293-418-1413 |
| 31 | 98.2 | 70.1 | 254 | 10 | US-09-880-748-1659 |
| 32 | 98.2 | 70.1 | 254 | 15 | US-10-293-418-1659 |
| 33 | 98.2 | 70.1 | 450 | 17 | US-10-484-790A-17 |
| 34 | 98.2 | 70.1 | 453 | 17 | US-10-484-790A-18 |
| 35 | 97.2 | 69.4 | 249 | 10 | US-09-880-748-957 |
| 36 | 97.2 | 69.4 | 249 | 15 | US-10-293-418-957 |
| 37 | 95 | 67.9 | 246 | 10 | US-09-880-748-1847 |
| 38 | 95 | 67.9 | 246 | 15 | US-10-293-418-1847 |
| 39 | 94.2 | 67.3 | 123 | 14 | US-10-269-805-31 |
| 40 | 94.2 | 67.3 | 123 | 14 | US-10-269-805-55 |
| 41 | 94.2 | 67.3 | 255 | 10 | US-09-880-748-1642 |
| 42 | 94.2 | 67.3 | 255 | 15 | US-10-293-418-1642 |
| 43 | 93.7 | 66.9 | 116 | 15 | US-10-308-817-189 |
| 44 | 93.7 | 66.9 | 116 | 15 | US-10-453-698-189 |
| 45 | 93.2 | 66.6 | 250 | 10 | US-09-880-748-993 |

ALIGNMENTS

RESULT 1
US-09-880-748-1333
; Sequence 1333, Appl
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

```
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.: 0.00155 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 1 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-880-748-1333 (1-253)

QY 3 GCGAGTCA-----GGATAT 17
Db 26 GlycylserPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
QY 18 TAGCAGCTGGTTAGCCGAATCAATAGTGGAAAGCACCACCACTACAAACCGTCCCTCAA 77
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
QY 78 GAGT 81
Db 64 sSer 65

RESULT 3
US-10-371-942-118
; Sequence 118, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-118

Alignment Scores:
Pred. No.: 0.00146 Length: 125
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 1 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-10-371-942-118 (1-125)

QY 3 GCGAGTCAAGTATTAGCAGC----- 24
Db 26 Glycylser-----IleSerSerSerSerTyrTrpAlaTrpIleArgGlnProProGl 44
QY 25 -----TGGTTAGCCGAATCAATCATAGTGGAAAGCACCACCACTACAAACCGTCC 71
Db 44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64
QY 72 CCTCAAGAGT 81
Db 64 rLeuLysSer 67

RESULT 4
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
```

```
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.: 0.00155 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 1 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-09-880-748-1333 (1-253)

QY 3 GCGAGTCA-----GGATAT 17
Db 26 GlycylserPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
QY 18 TAGCAGCTGGTTAGCCGAATCAATAGTGGAAAGCACCACCACTACAAACCGTCCCTCAA 77
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
QY 78 GAGT 81
Db 64 sSer 65

RESULT 2
US-10-293-418-1333
; Sequence 1333, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BLys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2002-11-16
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.: 0.00155 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 1 Gaps: 1

NOLAN463-1B.SEQ (1-81) x US-10-293-418-1333 (1-253)
```

TITLE OF INVENTION: HYBRID ANTIBODIES

US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:

US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:

```
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.: 0.00228      Length: 97
Score: 98.20           Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-029-988B-87 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
QY 62 ACAACCGGTCCTCAAGAGT 81
   |||
Db 59 YrAsnProSerLeuLysSer 65

RESULT 9
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.: 0.00228      Length: 97
Score: 98.20           Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-032-423A-87 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
QY 62 ACAACCGGTCCTCAAGAGT 81
   |||
Db 59 YrAsnProSerLeuLysSer 65
```

```
RESULT 10
US-10-453-698-83
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.: 0.00228      Length: 97
Score: 98.20           Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-453-698-83 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
QY 62 ACAACCGGTCCTCAAGAGT 81
   |||
Db 59 YrAsnProSerLeuLysSer 65

RESULT 11
US-10-029-926B-87
; Sequence 87, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.: 0.00228      Length: 97
Score: 98.20           Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-029-926B-87 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: |||
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
QY 62 ACAACCGGTCCTCAAGAGT 81
   |||
Db 59 YrAsnProSerLeuLysSer 65
```



```
RESULT 12
US-10-379-392-47
; Sequence 47, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-47

Alignment Scores:
Pred. No.: 0.00228 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 16 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-379-392-47 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61
Db 42 Glylys---GlyLeu---GlutrpIleGlyGlulieAenHisSerGlySerThrAenT 59

Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 59 yraenProSerLeuLysSer 65

RESULT 13
US-10-733-532-128
; Sequence 128, Application US/10733532
; Publication No. US20050026246A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2002B
; CURRENT APPLICATION NUMBER: US/10/733,532
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: PCT/GB02/02688
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 10/146,505
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-532-128

Alignment Scores:
Pred. No.: 0.00235 Length: 114
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 16 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-733-532-128 (1-114)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61
Db 42 Glylys---GlyLeu---GlutrpIleGlyGlulieAenHisSerGlySerThrAenT 59

Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 59 yraenProSerLeuLysSer 65

RESULT 14
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Wei
; APPLICANT: GALIBERT, Laurent J.
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.: 0.00235 Length: 115
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 17 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-898-408-12 (1-115)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61
Db 42 Glylys---GlyLeu---GlutrpIleGlyGlulieAenHisSerGlySerThrAenT 59

Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 59 yraenProSerLeuLysSer 65

RESULT 15
US-09-864-761-44315
; Sequence 44315, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
```

```
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 17 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-733-532-128 (1-114)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61
Db 36 Glylys---GlyLeu---GlutrpIleGlyGlulieAenHisSerGlySerThrAenT 53

Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 53 yraenProSerLeuLysSer 59

RESULT 14
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Wei
; APPLICANT: GALIBERT, Laurent J.
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.: 0.00235 Length: 115
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 17 Gaps: 0

NOLAN463-1B.SEQ (1-81) x US-10-898-408-12 (1-115)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61
Db 42 Glylys---GlyLeu---GlutrpIleGlyGlulieAenHisSerGlySerThrAenT 59

Qy 62 ACAACCCGTCCTCAAGAGT 81
Db 59 yraenProSerLeuLysSer 65

RESULT 15
US-09-864-761-44315
; Sequence 44315, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
```

```

; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44315
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019439.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
; OTHER INFORMATION: EST HUMAN HIT: BE672445.1, EVALUE 2.00e-57
; OTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 1.00e-53
US-09-864-761-44315

```

```

Alignment Scores:
Pred. No.: 0.00236 Length: 117
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 9 Gaps: 0

```

NOLAN463-1B.SEQ (1-81) x US-09-864-761-44315 (1-117)

```

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTAGCCGAAATCATCATAGTGGAGGACCAACT 61
Db 45 Glylys---GlyLeu---GluTrpIleGlyIleAsnHisSerGlySerThrAsnT 62
Qy 62 ACAACCGTCCTCAAGAGT 81
Db 62 YrAsnProSerLeuLySer 68

```

Search completed: August 4, 2005, 18:49:49
Job time : 81.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:04:24 ; Search time 18.25 Seconds
(without alignments)
854.089 Million cell updates/sec

Title: NOLAN463-LB.SEQ

Perfect score: 140

Sequence: 1 CGGGCGAGTCAGGATATTAG.....ACAACCGTCCTCAAGAGT 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_P/NOLAN08728463-1/runat_04082005_125806_24544/app_query.fasta_1.5
-DB=PIR -QPMF=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-LOCALALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=NOLAN08728463-1 @CNC 1.1 77 @runat_04082005_125806_24544 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 101.6 | 72.6 | 143 | 2 B49028 | Ig heavy chain V-I |
| 2 | 100.4 | 71.7 | 97 | 2 S26805 | Ig heavy chain V-I |
| 3 | 98.2 | 70.1 | 97 | 2 S26898 | Ig heavy chain V-I |
| 4 | 98.2 | 70.1 | 97 | 2 S26806 | Ig heavy chain V-I |
| 5 | 98.2 | 70.1 | 106 | 2 S37454 | Ig mu chain - huma |
| 6 | 98.2 | 70.1 | 122 | 2 J10047 | Ig heavy chain V-I |
| 7 | 98.2 | 70.1 | 126 | 2 S47010 | Ig heavy chain V-I |
| 8 | 98.2 | 70.1 | 140 | 2 S78052 | Ig heavy chain pre |
| 9 | 98.2 | 70.1 | 140 | 2 A49045 | Ig heavy chain V-I |
| 10 | 98.2 | 70.1 | 231 | 2 B23746 | Ig Fab region IV-J |
| 11 | 98 | 70.0 | 133 | 2 PS0341 | Ig heavy chain V-D |
| 12 | 94.2 | 67.3 | 97 | 2 G34964 | Ig heavy chain V-I |
| 13 | 92 | 65.7 | 98 | 2 S26905 | Ig heavy chain V-I |
| 14 | 92 | 65.7 | 145 | 2 S78055 | Ig heavy chain pre |

ALIGNMENTS

RESULT 1

B49028

Ig heavy chain V-IV region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C/Accession: B49028

R/Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur

Eur. J. Immunol. 21, 2355-2363, 1991

A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob

A/Reference number: A49028; MUID:92008140; PMID:1915549

A/Accession: B49028

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-143 <TIM>

A/Cross-references: GB:S64473; NID:G236906; PIDN:AAB20012.1; PID:G236907

A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines

A/Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBI:P:64472)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 0.00109 Length: 143
Score: 101.60 Matches: 19
Percent Similarity: 55.56% Conservatives: 1
Best Local Similarity: 52.78% Mismatches: 2
Query Match: 72.57% Indels: 14
DB: 2 Gaps: 0

NOLAN463-LB.SEQ (1-81) x B49028 (1-143)

Oy 2 GGCGGAGTCAGGATATTAGAGCTGGTTACCCGAATCATCATAGTGGAGGACCAACT 61

|||||

44 GlyArg-----GlutripiledGluileAenHieSerGlySerThraent 59

62 ACAACCGTCCTCAAGAGT 81

|||||

59 yrAenProSerLeuLysSer 65

Db

```
RESULT 2
S26805
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26805
R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A/Reference number: S26800; MUID:92201299; PMID:1348029
A/Accession: S26805
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <WEN>
A/Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 0.000153 Length: 97
Score: 100.40 Matches: 20
Percent Similarity: 43.40% Conservative: 3
Best Local Similarity: 37.74% Mismatches: 4
Query Match: 71.71% Indels: 26
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x S26805 (1-97)
QY 1 CGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
QY 22 -----AGCTGTTAGCCGAAATCAAT 42
Db 33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGlyGluIleAsn 52
QY 43 CATAGTGGAGCCCACTACACCCCTCCCTCAAGAGT 81
Db 53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26898; S12420
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26898
A/Molecule type: DNA
A/Residues: 1-97 <TOW>
A/Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A/Experimental source: Clone DP-63
R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.
A/Reference number: S09421; MUID:90059975; PMID:2511001
A/Accession: S12420
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-97 <SAN>
A/Cross-references: EMBL:X56364
A/Experimental source: V(H)4.2
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 0.000295 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0
```

```
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S26898 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGTAGCCGAAATCAATCATAGTGGAGCCCACT 61
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsn 59
QY 62 ACAACCCGTCCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 4
S26806
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26806
R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A/Reference number: S26800; MUID:92201299; PMID:1348029
A/Accession: S26806
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <WEN>
A/Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 0.000295 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S26806 (1-97)
QY 2 GGCGGAGTCAGGATATTAGCAGCTGTAGCCGAAATCAATCATAGTGGAGCCCACT 61
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsn 59
QY 62 ACAACCCGTCCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 5
S37454
Ig mu chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37454
R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A/Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from
A/Reference number: S37453
A/Accession: S37454
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <MCI>
A/Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin

Alignment Scores:
Pred. No.: 0.000297 Length: 106
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0
```

Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S37454 (1-106)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
||||: |||
Db 20 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 37
||||: |||
Qy 62 ACAACCCGTCCTCAAGAGT 81
||||: |||
Db 37 yrAsnProSerLeuLysSer 43
||||: |||

RESULT 6

JI0047

Ig heavy chain V region precursor (clone cR18) - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C:Accession: JI0047

R:Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.

J. Exp. Med. 167, 2011-2016, 1988

A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5

A:Reference number: JI0047; MUID:88258392; PMID:3133445

A:Accession: JI0047

A:Molecule type: mRNA

A:Residues: 1-122 <BAE>

A:Experimental source: T-cell line RPMI 8402

A:Note: the authors translated the reading frame which extends to the stop codon; the se

A:Note: this sequence belongs to the VH II subgroup

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 0.000299 Length: 122
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x JI0047 (1-122)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
||||: |||
Db 50 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 67
||||: |||

Qy 62 ACAACCCGTCCTCAAGAGT 81
||||: |||

Db 67 yrAsnProSerLeuLysSer 73
||||: |||

RESULT 7

S47010

Ig heavy chain V4.21-Unique-J5 region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S47010

R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.

submitted to the EMBL Data Library, July 1994

A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bir

A:Reference number: S47009

A:Accession: S47010

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-126 <MAH>

A:Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 0.0003 Length: 126
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S47010 (1-126)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
||||: |||
Db 42 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
||||: |||
Qy 62 ACAACCCGTCCTCAAGAGT 81
||||: |||
Db 59 yrAsnProSerLeuLysSer 65
||||: |||

RESULT 8

S78052

Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C:Accession: S78052; S23717

R:Harindranath, N.

submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78052

A:Molecule type: mRNA

A:Residues: 1-140 <HAR>

A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA83808.1; PID:G930118

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins

Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h

patient.

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23717

A:Molecule type: mRNA

A:Residues: 15-111 <HAW>

A:Cross-references: EMBL:X54441

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>

F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 0.000301 Length: 140
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S78052 (1-140)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
||||: |||
Db 56 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 73
||||: |||

Qy 62 ACAACCCGTCCTCAAGAGT 81
||||: |||

Db 73 yrAsnProSerLeuLysSer 79
||||: |||

RESULT 9

A49045

Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C:Accession: A49045

R:Grillot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Rassenti, L.Z.; Labaume, S.; Silverma

Eur. J. Immunol. 22, 1781-1788, 1992

A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i b1

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TON>
A:Cross-references: EMBL:Z12370; NID:g32960; PIDN:CAA78240.1; PID:g32961
A>Note: designated DP-70
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A>Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Accession number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12419
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <SAN>
A:Cross-references: EMBL:X56363
A>Note: designated 4.19
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00189 Length: 98
Score: 92.00 Matches: 21
Percent Similarity: 48.89% Conservative: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x S26905 (1-98)
QY 3 GGCAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy 44
QY 25 -----TGCTTAGCCGAAATCAATCATAGTGGAGCAGCAACTACAAACCGTCCCT 74
Db 44 sGlyLeuGluTrpIleGlyGluLeuTyHISerGlySerThrAsnTyRAsnProSerLe 64
QY 75 CAAGAGT 81
Db 64 uLySer 66

RESULT 14
S78055
Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78055; S23720
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78055
A:Molecule type: mRNA
A:Residues: 1-145 <HAR>
A:Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23720
A:Molecule type: mRNA
A:Residues: 18-115 <HAW>
A:Cross-references: EMBL:X54445
A>Note: the authors translated the codon GCA for residue 67 as Arg
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00193 Length: 145
Score: 92.00 Matches: 21

Percent Similarity: 48.89% Conservative: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x S78055 (1-145)
QY 3 GGCAGTCAGGATATTAGCAGC----- 24
Db 43 GlyGlySer-----IleSerSerSerAsnTrpTrpSerTrpValArgGlnProProGlyLy 61
QY 25 -----TGCTTAGCCGAAATCAATCATAGTGGAGCAGCAACTACAAACCGTCCCT 74
Db 61 sGlyLeuGluTrpIleGlyGluLeuTyHISerGlySerThrAsnTyRAsnProSerLe 81
QY 75 CAAGAGT 81
Db 81 uLySer 83

RESULT 15
S14474
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S14474
R:van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H.
submitted to the EMBL Data Library, November 1990
A:Reference number: S14474
A:Accession: S14474
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <ESJ>
A:Cross-references: EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PID:g1335354
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00437 Length: 97
Score: 89.20 Matches: 18
Percent Similarity: 62.50% Conservative: 2
Best Local Similarity: 56.25% Mismatches: 4
Query Match: 63.71% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x S14474 (1-97)
QY 2 GGCAGTCAGGATATTAGCAGCTGGTAGCCGAAATCAATCATAGTGGAGCAGCAACT 61
Db 42 GlyLys-----GlyLeu----GluTrpIleGlyGluIleHisSerGlySerThrAsn 59
QY 62 ACAACCGTCCTCAAGAGT 81
Db 59 yrAsnProSerLeuLySer 65

Search completed: August 4, 2005, 18:21:23
Job time : 18.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 17:55:57 ; Search time 83.75 Seconds
(without alignments)
990.529 Million cell updates/sec

Title: NOLAN463-LB.SEQ

Perfect score: 140

Sequence: 1 CGGCGAGTCAAGATATTAG.....ACAACCCGTCCTCAAGAGT 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/NOLAN08728463-1/runat.04082005.125806.24533/app_query.fasta_1.5
-DB=uniprot -OPMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-1 @CGN 1.1 305 @runat.04082005.125806.24533 -NCPU=6
-ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.1 -FGAPOP=6
-FGAEXT=0.1 -YGAPOP=10 -YGAEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| 1 | 98.2 | 70.1 | 116 | 2 | Q7Z3Y6 |
| 2 | 98.2 | 70.1 | 595 | 2 | Q8WUX4 |
| 3 | 98.2 | 70.1 | 597 | 2 | Q8GMX5 |
| 4 | 98.2 | 70.1 | 597 | 2 | Q9BU10 |
| 5 | 98.2 | 70.1 | 625 | 2 | Q96AA6 |
| 6 | 92.2 | 65.9 | 597 | 2 | Q9BQB8 |
| 7 | 92 | 65.7 | 576 | 2 | Q6P4I8 |
| 8 | 87.2 | 62.3 | 146 | 1 | HV21_HUMAN |
| 9 | 82.1 | 58.6 | 477 | 2 | Q8GMX7 |
| 10 | 79.1 | 56.5 | 139 | 2 | Q86SX2 |
| 11 | 77.1 | 55.1 | 620 | 2 | Q96EY0 |
| 12 | 76.3 | 54.5 | 479 | 2 | Q99M22 |
| 13 | 75.7 | 54.1 | 116 | 1 | HV61_MOUSE |
| 14 | 75.2 | 53.7 | 465 | 2 | Q6CM76 |
| 15 | 72.8 | 52.0 | 262 | 2 | Q65Z11 |
| 16 | 71.3 | 50.9 | 116 | 1 | HV60_MOUSE |

| | | | | | | |
|----|------|------|-----|---|------------|---------------------|
| 17 | 71.2 | 50.9 | 119 | 2 | Q9UL73 | Q9UL73 homo sapien |
| 18 | 71.2 | 50.9 | 476 | 2 | Q6GMX1 | Q6GMX1 homo sapien |
| 19 | 69.1 | 49.4 | 478 | 2 | Q6NYH3 | Q6NYH3 homo sapien |
| 20 | 68.6 | 49.0 | 150 | 2 | Q95973 | Q95973 homo sapien |
| 21 | 68.2 | 48.7 | 478 | 2 | Q7Z379 | Q7Z379 homo sapien |
| 22 | 67.4 | 48.1 | 113 | 1 | HV47_MOUSE | P01823 mus musculus |
| 23 | 66.4 | 47.4 | 104 | 2 | Q99CA9 | Q99CA9 human immun |
| 24 | 66.4 | 47.4 | 106 | 2 | Q6TJQ4 | Q6TJQ4 human immun |
| 25 | 66.4 | 47.4 | 133 | 2 | Q90QV6 | Q90QV6 human immun |
| 26 | 65.9 | 47.1 | 496 | 2 | Q96KX8 | Q96KX8 homo sapien |
| 27 | 65.5 | 46.8 | 523 | 2 | Q6QJ60 | Q6QJ60 paraphlegop |
| 28 | 65.5 | 46.8 | 523 | 2 | Q6QJ62 | Q6QJ62 paraphlegop |
| 29 | 65.4 | 46.7 | 104 | 2 | Q99CH3 | Q99CH3 human immun |
| 30 | 65.4 | 46.7 | 130 | 2 | Q9QL43 | Q9QL43 human immun |
| 31 | 65.4 | 46.7 | 202 | 2 | Q9IUP1 | Q9IUP1 human immun |
| 32 | 65.4 | 46.7 | 202 | 2 | Q9IUR6 | Q9IUR6 human immun |
| 33 | 65.4 | 46.7 | 206 | 2 | Q7ZN97 | Q7ZN97 human immun |
| 34 | 65.4 | 46.7 | 207 | 2 | Q9IIQ5 | Q9IIQ5 human immun |
| 35 | 65.4 | 46.7 | 212 | 2 | Q9J783 | Q9J783 human immun |
| 36 | 65.4 | 46.7 | 220 | 2 | Q9IUT6 | Q9IUT6 human immun |
| 37 | 65.4 | 46.7 | 231 | 2 | Q9IQS9 | Q9IQS9 human immun |
| 38 | 65.4 | 46.7 | 489 | 2 | Q80632 | Q80632 human immun |
| 39 | 65.3 | 46.6 | 136 | 2 | Q6LBQ5 | Q6LBQ5 mus musculus |
| 40 | 65.3 | 46.6 | 137 | 1 | HV45_MOUSE | P01822 mus musculus |
| 41 | 64.4 | 46.0 | 130 | 2 | Q7ZB82 | Q7ZB82 human immun |
| 42 | 64.4 | 46.0 | 131 | 2 | Q90QT5 | Q90QT5 human immun |
| 43 | 64.4 | 46.0 | 131 | 2 | Q9QKY2 | Q9QKY2 human immun |
| 44 | 64.4 | 46.0 | 131 | 2 | Q9QKY3 | Q9QKY3 human immun |
| 45 | 64.4 | 46.0 | 140 | 2 | Q698Z8 | Q698Z8 human immun |

ALIGNMENTS

RESULT 1
Q7Z3Y6 PRELIMINARY; PRT; 116 AA.
AC Q7Z3Y6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN Name=VH4-34;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauning A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -
DR HSP; P18532; IKCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12902 MW; CE3DBA84616C908 CRC64;

Alignment Scores:
Pred. No.: 0.000788 Length: 116
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-LB.SEQ (1-81) x Q7Z3Y6 (1-116)

Qy 2 GGGCGAGTCAGGATATTAGAGCTGGTTAGCCGGAATCAATCATAGTGGGAAGCACT 61

```
||||:| 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
||||:| 62 ACAACCGTCCCTCAAGAGT 81
||||:| 59 YrAnProSerLeuLysSer 65

RESULT 2
Q8WUX4 Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4; 2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; --
DR PIR; G34964; G34964.
DR HSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Alignment Scores:
Pred. No.: 0.000979 Length: 595
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B-SEQ (1-81) x Q8WUX4 (1-595)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGGAATCAATCATAGTGGAGCAACCACT 61
Db 68 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85
```

```
62 ACAACCGTCCCTCAAGAGT 81
||||:| 85 YrAnProSerLeuLysSer 91

RESULT 3
Q6GMX5 Q6GMX5 PRELIMINARY; PRT; 597 AA.
AC Q6GMX5; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.: 0.000979 Length: 597
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B-SEQ (1-81) x Q6GMX5 (1-597)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGGAATCAATCATAGTGGAGCAACCACT 61
```



```
||||:|
68 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85
||||:|
62 ACAACCGCTCCCTCAAGAGT 81
||||:|
85 YrAsnProSerLeuLysSer 91

RESULT 6
Q9BQB8 PRELIMINARY; PRT; 597 AA.
ID Q9BQB8
AC Q9BQB8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.: 0.00622 Length: 597
Score: 92.20 Matches: 18
Percent Similarity: 62.50% Conservative: 2
Best Local Similarity: 56.25% Mismatches: 4
Query Match: 65.86% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B.SEQ (1-81) x Q9BQB8 (1-597)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATGATGAGACCAACT 61
Db ||||:|
61 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
```

```
Qy 62 ACAACCGCTCCCTCAAGAGT 81
||||:|
Db 78 YrAsnProSerLeuLysSer 84

RESULT 7
Q6P418 PRELIMINARY; PRT; 576 AA.
ID Q6P418
AC Q6P418
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSP; P01820; IA7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 0.00658 Length: 576
Score: 92.00 Matches: 21
Percent Similarity: 48.89% Conservative: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x Q6P418 (1-576)
```

```

QY 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 52 GlyGlySer-----IleSerSerSerAsnTrpSerTrpVala:rgInProProGlyly 70
QY 25 -----TGCTTAGCCGAATCAATCATAGTGGAGCACCACCACTACACCCGTCCT 74
Db 70 sGlyLeuGluTrpIleGlyGluIleTyHisSerGlySerThrAsnTyAsnProSer 90
QY 75 CAAGAGT 81
Db 90 uLySer 92

RESULT 8
ID HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR; A02101; GIHUH2.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Alignment Scores:
Pred. No.: 0.024 Length: 146
Score: 87.20 Matches: 16
Percent Similarity: 59.38% Conservative: 1
Best Local Similarity: 56.25% Mismatches: 5
Query Match: 62.29% Indels: 8
DB: 1 Gaps: 0

NOLAN463-1B_SEQ (1-81) x HV21_HUMAN (1-146)

QY 2 GCGGAGTCAGGATATTAGCAGC----- 61
Db 62 GlyArg-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsn 79
QY 62 ACAACCCGTCCTCAAGT 81
Db 79 yzLysThrSerLeuLysSer 85

RESULT 9
Q6GMX7
ID Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;

```

```

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9PE59C09C50CFF85 CRC64;

Alignment Scores:
Pred. No.: 0.135 Length: 477
Score: 82.10 Matches: 19
Percent Similarity: 47.73% Conservative: 2
Best Local Similarity: 43.18% Mismatches: 4
Query Match: 58.64% Indels: 19
DB: 2 Gaps: 1

NOLAN463-1B_SEQ (1-81) x Q6GMX7 (1-477)

QY 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 45 GlyGlySer-----IleSerSerTyTrpSerTrpIleArgGlnThrAlaGlyLysG 63
QY 25 -----TGCTTAGCCGAATCAATCATAGTGGAGCACCACCACTACACCCGTCCTCAA 77
Db 63 yLeuGluTrpIleGlyTyIleSerHisSerGlySerThrThrTyAsnProSerLeu 83
QY 78 GAGT 81

```

RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN
RN SEQUENCE FROM N.A.
RP
RP TISSUE=Primary B-Cells;
RC
RC Strausberg R.;
RA
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSP; P01820; I67J.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG.MHC.
DR InterPro: IPR003596; IG.V.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG: 2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00405; IGLIKE; 5.
DR PROSITE; PS0835; IG.LIKE; 5.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 56125 NW; 990A1A4A6E8FE27B CRC64;

Alignment Scores:
Pred. No.: 0.654 Length: 620
Score: 77.10 Matches: 19
Percent Similarity: 45.45% Conservative: 1
Best Local Similarity: 43.18% Mismatches: 5
Query Match: 55.07% Indels: 19
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x Q96EY0 (1-620)

Qy 3 GCGAGCTCAGGATATTAGCAGC----- 24
Db 52 GlyGlySer-----IleSerSerTyTyTrpSerTrpIleargGlnProAlaGlyLysGI 70
Qy 25 -----TGGTTAGCGGAATCAATCATAGTGGAGCACCACCACTACACCGGTCCCTCAA 77
Db 70 yLeuGluTnTrpIleGlyArgIleTyThrSerGlySerThrAsnTyAsnProSerLeuLy 90
Qy 78 GAGT 81
Db 90 sSer 91

RESULT 12
Q99M22 PRELIMINARY; PRT; 479 AA.
ID AC Q99M22
AC Q99M22;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.

```

OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zerbe B., Bueckow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AH02091.1; --
DR HSSP; P01820; IG70.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 769E39A138918892 CRC64;

Alignment Scores:
Pred. No.: 0.808 Length: 479
Score: 76.30 Matches: 15
Percent Similarity: 37.04% Conservative: 5
Best Local Similarity: 27.78% Mismatches: 7
Query Match: 54.50% Indels: 27
DB: 2 Gaps: 1

NOLAN463-1B.SEQ (1-81) x Q99M22 (1-479)
QY 1 CGGGGAGTCAGATATTAGC-----AGCTGGTTAGCCGGAATC 39
Db 31 LysProSerGlnSerLeuSerLeuThrCysSerValThrGlyTySerIleThrSergly 50
QY 22 -----AGCTGGTTAGCCGGAATC 39
Db 51 TyrTyTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrlle 70
QY 40 AATCATAGTGGAGCACCACCACTACACCGTCCTCCCTCAAGAGT 81
Db 71 AsnTyAspGlySerAsnAsnTyAsnProSerLeuLysAsn 84

RESULT 13
HV61_MOUSE
ID HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499854;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
DR PIR; J70508; HVMS1B.
DR PDB; 1KCS; X-ray; Hs19-116.
DR PDB; 1KCV; X-ray; Hs19-116.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 Ig heavy chain V region 1B43.
FT DOMAIN 19 48 Framework-1.
FT DOMAIN 49 53 Complementarity-determining-1.
FT DOMAIN 54 67 Framework-2.
FT DOMAIN 68 84 Complementarity-determining-2.
FT DOMAIN 85 116 Framework-3.
FT DISULFID 40 114 By similarity.
FT STRAND 21 25
FT STRAND 29 30
FT TURN 32 33
FT STRAND 36 43
FT TURN 47 49
FT TURN 52 58
FT TURN 60 61
FT STRAND 64 71
FT TURN 72 73
FT STRAND 76 78
FT TURN 80 85
FT STRAND 86 91
FT TURN 92 95
FT STRAND 96 101
FT HELIX 106 108
FT STRAND 110 116
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Alignment Scores:
Pred. No.: 0.805 Length: 116
Score: 75.70 Matches: 16
Percent Similarity: 56.76% Conservative: 5
Best Local Similarity: 43.24% Mismatches: 3
Query Match: 54.07% Indels: 13
DB: 1 Gaps: 1

NOLAN463-1B.SEQ (1-81) x HV61_MOUSE (1-116)
QY 9 TCAGATATTAGC-----AGCTGGTTAGC 32
Db 49 SerGlyTyTrpSerTrpHisTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetG1 68
QY 33 CGAATCAATCATAGTGGAGCACCACCACTACACCGTCCTCCCTCAAGAGT 81
Db 68 yTyrlleHisTySerGlyAsnThrSertyrAsnProSerLeuLysSer 84

RESULT 14
HV61_MOUSE
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

```

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam: PF07654; Cl-set; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores:
Pred. No.: 1.13 Length: 465
Score: 75.20 Matches: 16
Percent Similarity: 56.25% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 53.71% Indels: 8
DB: 2 Gaps: 0

NOLAN463-1B_SEQ (1-81) x Q6GMX6 (1-465)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTAGCCGAATCAATCATATAGTCGAGCACCACACT 61
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
61 GlyLys----GlyLeu----GluTrpIleGlyArgIleTyrThrSerGlySerThrAsnT 78
QY 62 ACAACCCGTCCTCAAGAGT 81
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
78 YrAsnProSerLeuLysSer 84

RESULT 15
Q65Z11
ID Q65Z11 PRELIMINARY; PRT; 262 AA.
AC Q65Z11;
```

```
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-HIV-1 reverse transcriptase single-chain variable.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=96211469; PubMed=8648670;
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT "targeting human immunodeficiency virus type 1 reverse transcriptase
by intracellular expression of single-chain variable fragments to
inhibit early stages of the viral life cycle.";
RL J. Virol. 70:3392-3400(1996).
DR EMBL: U48716; AAB64342.1; -.
DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;

Alignment Scores:
Pred. No.: 2.19 Length: 262
Score: 72.80 Matches: 16
Percent Similarity: 55.56% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 4
Query Match: 52.00% Indels: 12
DB: 2 Gaps: 1

NOLAN463-1B_SEQ (1-81) x Q65Z11 (1-262)

QY 9 TCAGGATATTAGCAGCTGGTTAGCCGAA----- 36
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
178 SerGlyTyr-TrpAsnTrpIleArgLysPheProGlyAsnLysLeuAspTyrMetGlyTy 197
QY 37 -ATCAATCATAGTCGAGCACCACCACTACACCCGTCCTCAAGAGT 81
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
197 rIleAsnTyrSerGlyAspThrTyrTyrAsnProSerLeuLysSer 212

Search completed: August 4, 2005, 18:20:08
Job time : 85.75 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:21:34 ; Search time 90 Seconds
(without alignments)
721.953 Million cell updates/sec

Title: NOLAN463-2A.SEQ

Perfect score: 148

Sequence: 1 ATCATCTATCTGCTGACTC.....GTATTAGCAGCTGGTTAGCC 84

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cn2.1/USPTO.spool.p/NOLAN08728463-2/runat_04082005_123943_22574/app.query.fasta_1.5
-DB=A_Geneseq -OFT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNIT5=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1.1 308 @runat_04082005_123943_22574 -NCPU=6
-ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : A_Geneseq_16Dec04.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 114.1 | 77.1 | 240 | AAV15128 | Aav15128 Anti-muri |
| 2 | 104.9 | 70.9 | 302 | AAE70844 | Aae70844 SNV-env 1 |
| 3 | 97.9 | 66.1 | 116 | AAH48005 | Aam48005 Human mon |
| 4 | 97.9 | 66.1 | 116 | ADR46821 | Adr46821 Human ant |
| 5 | 97.9 | 66.1 | 411 | ADR46829 | Adr46829 Human pB1 |
| 6 | 97.9 | 66.1 | 468 | ADR46819 | Adr46819 Human ant |
| 7 | 97.9 | 66.1 | 613 | ADR46827 | Adr46827 Human bet |
| 8 | 95.2 | 65.0 | 118 | ADP47114 | Adp47114 Human pho |
| 9 | 95.4 | 64.5 | 129 | ADK18605 | Adk18605 Anti-huma |
| 10 | 95.4 | 64.5 | 129 | ADK18791 | Adk18791 Anti-huma |

| | | | | | | |
|----|------|------|-----|---|----------|--------------------|
| 11 | 95.4 | 64.5 | 129 | 7 | ADK18895 | Adk18895 Anti-huma |
| 12 | 95.4 | 64.5 | 129 | 7 | ADK18826 | Adk18826 Anti-huma |
| 13 | 95.4 | 64.5 | 129 | 8 | ADL25428 | Adl25428 Human mAb |
| 14 | 94.9 | 64.1 | 116 | 8 | ADP22194 | Adp22194 Human ant |
| 15 | 93.8 | 63.4 | 118 | 8 | ADP47088 | Adp47088 Human pho |
| 16 | 93.5 | 63.2 | 118 | 8 | ADP47090 | Adp47090 Human pho |
| 17 | 93.5 | 63.2 | 118 | 8 | ADP47098 | Adp47098 Human pho |
| 18 | 93.5 | 63.2 | 118 | 8 | ADP47224 | Adp47224 Human pho |
| 19 | 93.5 | 63.2 | 245 | 4 | AAE67621 | Aae67621 Human leu |
| 20 | 93.2 | 63.0 | 123 | 5 | ABG76561 | Abg76561 HCV E1 an |
| 21 | 92.4 | 62.4 | 225 | 6 | ABR01521 | AbR01521 Human ant |
| 22 | 92.2 | 62.3 | 84 | 2 | AAW62797 | Aaw62797 Amino aci |
| 23 | 92.2 | 62.3 | 98 | 5 | ABG78233 | Abg78233 Human Fv |
| 24 | 92.2 | 62.3 | 98 | 5 | ABG78231 | Abg78231 Human Fv |
| 25 | 92.2 | 62.3 | 98 | 5 | ABG91924 | Abg91924 Human ant |
| 26 | 92.2 | 62.3 | 98 | 5 | ABG91922 | Abg91922 Human ant |
| 27 | 92.2 | 62.3 | 98 | 6 | ABP56508 | Abp56508 Human ant |
| 28 | 92.2 | 62.3 | 98 | 6 | ABJ18687 | Abj18687 Antibody |
| 29 | 92.2 | 62.3 | 98 | 6 | ABO27112 | ABO27112 Human ger |
| 30 | 92.2 | 62.3 | 98 | 7 | ADD69247 | Add69247 Human hea |
| 31 | 92.2 | 62.3 | 98 | 7 | ADF10156 | Adf10156 Antibody |
| 32 | 92.2 | 62.3 | 98 | 7 | ADF09948 | Adf09948 Antibody |
| 33 | 92.2 | 62.3 | 98 | 7 | ADF10053 | Adf10053 VEGF anti |
| 34 | 92.2 | 62.3 | 98 | 7 | ADK18943 | Adk18943 Anti-huma |
| 35 | 92.2 | 62.3 | 98 | 7 | ADK18888 | Adk18888 Anti-huma |
| 36 | 92.2 | 62.3 | 98 | 7 | ADK18877 | Adk18877 Anti-huma |
| 37 | 92.2 | 62.3 | 98 | 7 | ADK18878 | Adk18878 Anti-huma |
| 38 | 92.2 | 62.3 | 98 | 7 | ADK18912 | Adk18912 Anti-huma |
| 39 | 92.2 | 62.3 | 98 | 7 | ADK18582 | Adk18582 Anti-huma |
| 40 | 92.2 | 62.3 | 98 | 7 | ADK18890 | Adk18890 Anti-huma |
| 41 | 92.2 | 62.3 | 98 | 7 | ADK18896 | Adk18896 Anti-huma |
| 42 | 92.2 | 62.3 | 98 | 7 | ADK18894 | Adk18894 Anti-huma |
| 43 | 92.2 | 62.3 | 98 | 7 | ADK18914 | Adk18914 Anti-huma |
| 44 | 92.2 | 62.3 | 98 | 7 | ADJ80328 | Adj80328 VH gene 1 |
| 45 | 92.2 | 62.3 | 98 | 8 | ADR46847 | Adr46847 Human VH5 |

ALIGNMENTS

RESULT 1

AAV15128

ID AAV15128 standard; protein; 240 AA.

XX AC AAV15128;

XX DT 07-FEB-2000 (first entry)

XX DE Anti-murine CTLA-4 M24 sFv.

XX KW Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4;

XX KW membrane-associated protein; chimeric construct; extracellular domain;

XX KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;

XX KW recipient CD28; T-cell proliferation;

XX KW xenograft-specific immunosuppression.

XX OS Mus sp.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 153 /note= "Corresponds to atc codon"

XX FT

XX PN WO9957266-A2.

XX PD 11-NOV-1999.

XX PF 30-APR-1999; 99WO-GB001350.

XX PR 30-APR-1998; 98GB-00009280.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PX Lechler-IR, Dorling A;

XX WPI; 2000-039815/03.
 DR N-PSDB; AAZ29000.
 XX
 PT Inhibiting T-cell mediated rejection of xenotransplanted organs.
 XX
 PS Claim 9; Fig 11; 43pp; English.
 XX
 CC The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a
 CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
 CC comprising DNA sequences encoding the extracellular domain of murine
 CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
 CC The anti-CTLA4 sFv functions as a ligand binding to CTLA-4 on activated
 CC T-cells and antagonises the co-stimulatory signal provided by the
 CC interaction between donor B7 and recipient CD28. Cells expressing the
 CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
 CC xenograft-specific immunosuppression
 XX
 SQ Sequence 240 AA;

Alignment Scores:
 Pred. No.: 0.000165 Length: 240
 Score: 114.10 Matches: 26
 Percent Similarity: 23.08% Conservative: 1
 Best Local Similarity: 22.22% Mismatches: 1
 Query Match: 77.09% Indels: 89
 DB: 3 Gaps: 1

NOLAN463-2A.SEQ (1-84) x AAY15128 (1-240)

QY 1 ATCATCTATCTCGTGACTCTGATACACATACAGCCGCTCTTCCRAAGGC----- 51
 DB 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
 QY 51 ----- 51
 DB 70 lIeSerAlaAspLySerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
 QY 51 ----- 51
 DB 90 AspThrAlaValTyrTyrCysAlaArgPheSerLeuGlyGlyPheAspTyrTrpGlyGln 109
 QY 51 ----- 51
 DB 110 GlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGly 129
 QY 51 ----- 51
 DB 130 SerAlaLeuAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerValGlyAsp 149
 QY 52 -----CGGCGAGTCAGGTATTACAGCTGTTAGCC 84
 DB 150 ArgValThrThrCysArgAlaSerGlnGlyIleSerSerTyrLeuAla 166

RESULT 2

AAB70844

ID AAB70844 standard; protein; 302 AA.

XX

AC AAB70844;

XX

DT 11-SEP-2003 (revised)

DT 25-JUN-2001 (first entry)

DE SNV-env leader/human 6C3-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct.

OS Homo sapiens.

OS Spleen necrosis virus.

OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..45
 FT /label= SNV-env_leader
 FT Protein 46..302
 FT /label= 6C3-scFv
 XX
 PN DE19946142-A1.
 XX
 XX 29-MAR-2001.
 PD
 XX
 PF 27-SEP-1999; 99DE-01046142.
 XX
 PR 27-SEP-1999; 99DE-01046142.
 XX
 XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
 PA
 XX Cichutek K, Engelstaedter M;
 PI
 XX WPI; 2001-246140/26.
 DR
 DR N-PSDB; AAF61513.

Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment.

PS Claim 1; Fig 5; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a DNA sequence (I) encoding a single-chain variable antibody fragment (scFv). The products of the invention have antiviral, cytostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of T cell-associated diseases, specifically acquired immune deficiency syndrome (AIDS), severe combined immune deficiency (SCID) or T cell lymphoma. (A) target T cells, independently of the CD4 receptor, with high selectivity, 4-5 fold selectivity over human B cells, and 1000 fold selectivity over other human cells. A vector designated 7A5 encodes a 329 amino acid single-chain variable antibody fragment, fully defined in the specification. It was used to transform D17 (canine osteosarcoma cells susceptible to spleen necrosis virus (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transfection. The viral titer (infectious units/ml) was over 1 million for D17, 1 million for C8166 but less than 100 for HeLa, showing the high selectivity for human T cells. This sequence represents the SNV-env leader/human 6C3-scFv fusion construct used in the construction of novel cell targeting vectors described in the invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 302 AA;

Alignment Scores:
 Pred. No.: 0.00218 Length: 302
 Score: 104.90 Matches: 23
 Percent Similarity: 19.38% Conservative: 2
 Best Local Similarity: 17.83% Mismatches: 3
 Query Match: 70.88% Indels: 101
 DB: 4 Gaps: 1

NOLAN463-2A.SEQ (1-84) x AAB70844 (1-302)

QY 1 ATCATCTATCTCGTGACTCTGATACACATACAGCCGCTCTTCCRAAGGC----- 51
 DB 97 LeuileTyrProGlyAspSerAspThrLysTyrSerProSerPheGlnGlyGlnValThr 116
 QY 51 ----- 51
 DB 117 lIeSerAlaAspLySerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 136
 QY 51 ----- 51
 DB 137 AspThrAlaMetTyrTyrCysAlaArgValSerGlyTyrCysSerSerThrSerCysTyr 156

QY 51 ----- 51
 Db 157 AspTyrTyrTyrTyrMetAspValTrpGlyArgGlyThrLeuValThrValSerArg 176
 QY 51 ----- 51
 Db 177 GlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerAspIleValMetThr 196
 QY 52 -----CGGGCG 57
 Db 197 GlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrMetThrCysArgAla 216
 QY 58 ACTCAGGTATTAGCAGCTGTTAGCC 84
 Db 217 SerGlnAsnIleAsnIleTrpLeuAla 225
 RESULT 3
 AAM48005
 ID AAM48005 standard; protein; 116 AA.
 XX AC
 XX AAM48005;
 XX AC
 DT 08-MAR-2002 (first entry)
 XX Human monoclonal antibody B11 variable heavy chain protein.
 DE Human; monoclonal antibody; B11; antigen binding portion; dendritic cell;
 KW mannose receptor; growth; cytolysis; pathogen; virus; bacterium;
 KW autoimmune disease; inflammatory disorder; rheumatoid arthritis;
 KW multiple sclerosis; diabetes mellitus; immunomodulatory;
 KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
 KW antidiabetic; antianaemic; endocrine; dermatological; antithyroid;
 KW uropathic; ophthalmological; muscular.
 XX Homo sapiens.
 XX WO200185799-A2.
 XX 15-NOV-2001.
 XX 08-MAY-2001; 2001WO-US015114.
 XX 08-MAY-2000; 2000US-0203126P.
 PR 07-SEP-2000; 2000US-0230739P.
 XX (MEDA-) MEDAREX INC.
 PA Deo YM, Keler T;
 XX WPI; 2002-089788/12.
 DR N-PSDB; ABA05500.
 XX New human monoclonal antibodies specific for dendritic cells, useful for
 PT inhibiting growth or inducing cytolysis of a dendritic cell and treating
 PT or preventing a dendritic cell mediated disease, e.g., autoimmune
 PT disorders.
 XX Example 2; Fig 13; 95pp; English.
 PS The invention relates to human monoclonal antibodies or their antigen
 XX binding portions that specifically bind to dendritic cells and has one or
 CC more of the following characteristics: (a) a binding affinity constant to
 CC a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability
 CC to opsonise a dendritic cell; (c) the ability to internalise after
 CC binding to dendritic cells; or (d) the ability to activate dendritic
 CC cells. The isolated human monoclonal antibody or its antigen binding
 CC portion may also have any of the following characteristics: (a) mediates
 CC cytolysis of dendritic cells in the presence of human effector cells; or
 CC (b) inhibits growth of dendritic cells. The antibodies or its antigen
 CC binding portion, binds to and blocks the human mannose receptor on
 CC dendritic cells. The antibodies have immunomodulatory, antiinflammatory,
 CC antirheumatic, antiarthritic, neuroprotective, antidiabetic, antianaemic,

CC endocrine, dermatological, antithyroid, uropathic, ophthalmological and
 CC muscular activity. The antibodies or their antigen-binding fragments are
 CC useful for inhibiting growth of a dendritic cell, inducing cytolysis of a
 CC dendritic cell, treating or preventing a dendritic cell mediated disease,
 CC detecting the presence of a dendritic cell, targeting an antigen to a
 CC dendritic cell, and preventing binding of a pathogen (a virus or a
 CC bacterium) to human mannose receptor on dendritic cells. In particular,
 CC the antibodies may be used to treat, autoimmune disease, graft versus
 CC host disease, immune system or inflammatory disorders (e.g. rheumatoid
 CC arthritis), multiple sclerosis, diabetes mellitus, myasthenia gravis,
 CC pernicious anaemia, Addison's disease, lupus erythematosus, Reiter's
 CC syndrome and Graves disease. The present sequence is that of the human
 CC monoclonal antibody B11 variable heavy chain, useful to the invention
 XX
 SQ Sequence 116 AA;

Alignment Scores:

Pred. No.: 0.0111 Length: 116
 Score: 97.90 Matches: 19
 Percent Similarity: 36.84% Conservative: 2
 Best Local Similarity: 33.33% Mismatches: 5
 Query Match: 66.15% Indels: 31
 DB: 5 Gaps: 1

NOLAN463-2A.SEQ (1-84) x AAM48005 (1-116)

QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCAAGGC----- 51
 |||||
 Db 50 lleileTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 69
 |||||
 QY 51 ----- 51
 Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
 QY 52 -----CGGGCGAGTCAGGCTATTAGCAGCTGG 78
 |||||
 Db 90 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 106
 |||||

RESULT 4

ADR46821
 ID ADR46821 standard; protein; 116 AA.
 XX ADR46821;
 AC ADR46821;
 XX 18-NOV-2004 (first entry)
 DT Human antibody B11 heavy chain variable region protein SEQ ID NO:4.
 DE molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; heavy chain variable region.
 XX Homo sapiens.
 OS
 XX WO2004074432-A2.
 XX 02-SEP-2004.
 XX 30-JAN-2004; 2004WO-US002725.
 XX 31-JAN-2003; 2003US-0443979P.
 PR (MEDA-) MEDAREX INC.
 XX Keler T, Endres M, He L, Ramakrishna V;
 XX WPI; 2004-635555/61.
 DR N-PSDB; ADR46820.

XX New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
XX
PS Claim 11; SEQ ID NO 4; 82pp; English.
XX
XX The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADRA6847, or ADRA6849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADRA6829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human antibody B11 heavy chain
CC variable region, which is used in the exemplification of the present
CC invention.
XX

SQ Sequence 116 AA;

Alignment Scores:
Pred. No.: 0.0111 Length: 116
Score: 97.90 Matches: 19
Percent Similarity: 36.84% Conservatives: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 66.15% Indels: 31
DB: 8 Gaps: 1

NOLAN463-2A.SEQ (1-84) x ADRA6821 (1-116)

QY 1 ATCATCTATCTGGTGAATGATACACATACACCGCTCTTCCAGGC----- 51
Db 50 IletileTyProGlyAspSerAspThrIleTySerProSerPheGlnGlyClnValThr 69
QY 51 ----- 51
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGCGAGTCAGGGGTATTAGCAGCTGG 78
Db 90 AspThrAlaMetTyTyCysThrArgGlyAspArgGlyValAspTyTrp 106
||| ||| :|||: |||

RESULT 5
ADR46829
ID ADR46829 standard; protein; 411 AA.

AC ADR46829;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.
XX
XX
KW molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW betahCG; beta chorionic gonadotropin; antibody;
KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW antibody B11; pB11-betahCG molecular conjugate; fusion protein.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO2004074432-A2.
XX
XX 02-SEP-2004.
XX
XX 30-JAN-2004; 2004WO-US002725.
XX
XX 31-JAN-2003; 2003US-0443979P.
XX
XX (MEDA-) MEDAREX INC.
XX
XX Keler T, Endres M, He L, Ramakrishna V;
XX
XX MPI; 2004-635555/61.
XX
XX N-PSDB; ADR46828.
XX
XX New molecular conjugate having a monoclonal antibody that binds to human
PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT cytotoxic T cell response in cancers and infectious diseases.
XX
XX Claim 16; SEQ ID NO 12; 82pp; English.

The present invention describes a molecular conjugate comprising a
monoclonal antibody that binds to human antigen presenting cells (APCs)
linked to beta human chorionic gonadotropin (betahCG), where the antibody
comprises a heavy and/or light chain variable region derived from a human
VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
of SEQ ID NO:30 or 32 (ADRA6847, or ADRA6849), respectively. Also
described: (1) a molecular conjugate comprising a human antibody heavy
chain and a human antibody light chain, where either or both chains are
linked to betahCG; (2) a molecular conjugate comprising a human single
chain antibody that binds to human APCs linked to betahCG, where the
conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
(ADRA6829); (3) a composition comprising any of the molecular conjugates
as described above, and a carrier, optionally in combination with an
adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
against betahCG, comprising contacting any of the molecular conjugates
described above with APCs such that the antigen is processed and
presented to T cells in a manner which induces or enhances a T cell-
mediated response against the antigen; (5) immunising a subject
comprising administering any of the molecular conjugates described above,
optionally in combination with an adjuvant, a cytokine which stimulates
proliferation of dendritic cells and/or an immunostimulatory agent; and
(6) inducing or enhancing a cytotoxic T cell response against an antigen,
comprising forming a conjugate of the antigen and a monoclonal antibody
which binds to APCs, and contacting the conjugate either in vivo or ex
vivo with APCs such that the antigen is internalised, processed and
presented to T cells in a manner which induces or enhances a cytotoxic T
cell response against the antigen. The molecular conjugate has
cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
virucide and antimalarial activities, and can be used as a CD8 agonist,
and in vaccines. The methods and compositions of the present invention
are useful for inducing a cytotoxic T cell response, and in particular
for treating autoimmune disorders, cancers and infectious diseases by
eliciting a potent antigen-specific cytotoxic T lymphocyte response,
including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and

CC herpes. The present sequence represents a human pB11-betahCG molecular
 CC conjugate, which is used in the exemplification of the present invention.

XX Sequence 411 AA;

Alignment Scores:
 Pred. No.: 0.0162 Length: 411
 Score: 97.90 Matches: 19
 Percent Similarity: 36.84% Conservative: 2
 Best Local Similarity: 33.33% Mismatches: 5
 Query Match: 66.15% Indels: 31
 DB: 8 Gaps: 1

NOLAN463-2A.SEQ (1-84) x ADR46829 (1-411)

QY 1 ATCATCTATCTCGGTGACTCTGATACACATACAGCCGCTCTTCCAGGC----- 51
 |||||
 Db 191 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 210
 |||||
 QY 51 ----- 51

Db 211 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 230

QY 52 -----CGGCGAGTCAGGCTATTAGCAGCTGG 78
 |||||

Db 231 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 247
 |||||

RESULT 6

ADR46819

ID ADR46819 standard; protein; 468 AA.

XX ADR46819;

XX 18-NOV-2004 (first entry)

XX Human antibody B11 heavy chain variable region protein SEQ ID NO:2.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
 KW antibody B11; heavy chain variable region.

XX Homo sapiens.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADR46818.

XX New molecular conjugate having a monoclonal antibody that binds to human
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a
 PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 13; SEQ ID NO 2; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
 CC comprises a heavy and/or light chain variable region derived from a human

CC VHS-51 or Vx-I15 germline sequence with the 98 or 95 amino acid sequences
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
 CC described: (1) a molecular conjugate comprising a human antibody heavy
 CC chain and a human antibody light chain, where either or both chains are
 CC linked to betahCG; (2) a molecular conjugate comprising a human single
 CC chain antibody that binds to human APCs linked to betahCG, where the
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
 CC (ADR46829); (3) a composition comprising any of the molecular conjugates
 CC as described above, and a carrier, optionally in combination with an
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
 CC against betahCG, comprising contacting any of the molecular conjugates
 CC described above with APCs such that the antigen is processed and
 CC presented to T cells in a manner which induces or enhances a T cell-
 CC mediated response against the antigen; (5) immunising a subject
 CC comprising administering any of the molecular conjugates described above,
 CC optionally in combination with an adjuvant, a cytokine which stimulates
 CC proliferation of dendritic cells and/or an immunostimulatory agent; and
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
 CC comprising forming a conjugate of the antigen and a monoclonal antibody
 CC which binds to APCs, and contacting the conjugate either in vivo or ex
 CC vivo with APCs such that the antigen is internalised, processed and
 CC presented to T cells in a manner which induces or enhances a cytotoxic T
 CC cell response against the antigen. The molecular conjugate has
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,
 CC and in vaccines. The methods and compositions of the present invention
 CC are useful for inducing a cytotoxic T cell response, and in particular
 CC for treating autoimmune disorders, cancers and infectious diseases by
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
 CC herpes. The present sequence represents a human antibody B11 heavy chain
 CC variable region, which is used in the exemplification of the present
 CC invention.

XX

XX

SQ

Sequence 468 AA;

Alignment Scores:

Pred. No.: 0.0168 Length: 468
 Score: 97.90 Matches: 19
 Percent Similarity: 36.84% Conservative: 2

Best Local Similarity: 33.33% Mismatches: 5

Query Match: 66.15% Indels: 31

DB: 8 Gaps: 1

NOLAN463-2A.SEQ (1-84) x ADR46819 (1-468)

QY 1 ATCATCTATCTCGGTGACTCTGATACACATACAGCCGCTCTTCCAGGC----- 51
 |||||
 Db 69 IleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88
 |||||
 QY 51 ----- 51

Db 89 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108

QY 52 -----CGGCGAGTCAGGCTATTAGCAGCTGG 78
 |||||

Db 109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125
 |||||

RESULT 7

ADR46827

ID ADR46827 standard; protein; 613 AA.

XX ADR46827;

XX 18-NOV-2004 (first entry)

XX Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;
 KW betahCG; beta chorionic gonadotropin; antibody;
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;


```
DB: 8 Gaps: 2
NOLAN463-2A.SEQ (1-84) x ADP47114 (1-118)
QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAGGCGG----- 54
Db 50 llelleTyProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 55 -----GCCAGTTCAGGTATTAGCAGC-----TGG 78
Db 70 lleSerAlaAspGlnSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 9
ADK18605
ID ADK18605 standard; protein; 129 AA.
XX AC ADK18605;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-human PDGF-D antibody heavy chain protein sequence.
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX OS Homo sapiens.
XX PN WO2003057857-A2.
XX PD 17-JUL-2003.
XX PF 06-JAN-2003; 2003WO-US000398.
XX PR (ABGE-) ABGENIX INC.
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX DR WPI; 2003-587119/55.
XX PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX PS Disclosure; SEQ ID NO 29; 255pp; English.
XX CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX SQ Sequence 129 AA;
Alignment Scores:
Pred. No.: 0.0228 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: Gaps: 1
NOLAN463-2A.SEQ (1-84) x ADK18605 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAGGCGGCGAGT 60
Db 50 llelleTyProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69
RESULT 11
ADK18895
```

```
QY 61 CAGGTATTAGCAGC-----TGG 78
Db 70 -----lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 10
ADK18791
ID ADK18791 standard; protein; 129 AA.
XX AC ADK18791;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-human PDGF-D antibody protein related sequence #17.
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX OS Homo sapiens.
XX PN WO2003057857-A2.
XX PD 17-JUL-2003.
XX PF 06-JAN-2003; 2003WO-US000398.
XX PR 07-JAN-2002; 2002US-00041860.
XX PA (ABGE-) ABGENIX INC.
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX DR WPI; 2003-587119/55.
XX PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX PS Disclosure; SEQ ID NO 215; 255pp; English.
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX SQ Sequence 129 AA;
Alignment Scores:
Pred. No.: 0.0228 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: Gaps: 1
NOLAN463-2A.SEQ (1-84) x ADK18791 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAGGCGGCGAGT 60
Db 50 llelleTyProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnAlaThr 69
RESULT 11
ADK18895
```


OS Homo sapiens.
 XX WO2004024098-A2.
 XX 25-MAR-2004.
 XX 16-SEP-2003; 2003WO-US029414.
 XX 16-SEP-2002; 2002US-0411137P.
 XX (ABGE-) ABGENIX INC.
 XX (CURA-) CURAGEN CORP.
 XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
 XX WPI; 2004-269881/25.
 XX N-PSDB; ADL25427.
 XX Use of an antibody or its binding fragment that binds platelet derived
 PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
 PT nephritis.
 XX Disclosure; SEQ ID NO 38; 115pp; English.
 XX The present invention describes an antibody or its binding fragment that
 CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
 CC useful in preparing a medicament for treating nephritis. Also described:
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
 CC of treating mesangial proliferative glomerulonephritis. The antibody has
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
 CC antidiabetic activities, and can be used in gene therapy. The antibody or
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a
 CC medicament for treating nephritis and related disorders, e.g., mesangial
 CC proliferative glomerulonephritis. The present sequence represents a human
 CC monoclonal antibody (mab) variable region sequence, which is used in the
 CC exemplification of the present invention.
 XX SQ Sequence 129 AA;
 Alignment Scores:
 Pred. No.: 0.0228 Length: 129
 Score: 95.40 Matches: 20
 Percent Similarity: 57.50% Conservative: 3
 Best Local Similarity: 50.00% Mismatches: 1
 Query Match: 64.46% Indels: 16
 DB: 8 Gaps: 1
 NOLAN463-2A.SEQ (1-84) x ADL25428 (1-129)
 Qy 1 ATCATCTATCTGGTGACTCTGTACACATACAGCCGTCCTTCCAGGCGGCGAGT 60
 Db 50 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnAlaThr 69
 Qy 61 CAGGTAATTAGCAGC-----TG 78
 Db 70 -----lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 83
 RESULT 14
 ADP22194
 ID ADP22194 standard; protein; 116 AA.
 XX AC ADP22194;
 XX 09-SEP-2004 (first entry)
 XX Human anti-TNFA antibody light chain variable region SEQ ID NO:100.
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antineumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX Homo sapiens.
 OS WO2004050683-A2.
 XX PN 17-JUN-2004.
 XX PD 02-DEC-2003; 2003WO-US038281.
 XX PF 02-DEC-2002; 2002US-0430729P.
 XX PR (ABGE-) ABGENIX INC.
 XX PA Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 XX PI Haak-Frendscho M, Rathanaasami P, Pigott C, Liang ML, Lee R;
 XX PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 XX DR N-PSDB; ADP22193.
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX Example 10; SEQ ID NO 100; 213pp; English.
 XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDRI) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDRI having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFA induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antineumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX SQ Sequence 116 AA;
 Alignment Scores:
 Pred. No.: 0.0253 Length: 116
 Score: 94.90 Matches: 19
 Percent Similarity: 36.84% Conservative: 2
 Best Local Similarity: 33.33% Mismatches: 5
 Query Match: 64.12% Indels: 31

```
DB: 8 Gaps: 1
NOLAN463-2A.SEQ (1-84) x ADP22194 (1-116)
Qy 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAGGC----- 51
   |||||
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
   |||||
Qy 51 ----- 51
Db 70 IleSerAlaAspLysSerIleThrThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
Qy 52 -----CGGCGGAGTCAGGCTATTAGCAGCTGG 78
   |||||
Db 90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp 106
   |||||

RESULT 15
ADP47088
ID ADP47088 standard; protein; 118 AA.
XX
AC ADP47088;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human phospholipase A2-specific monoclonal antibody heavy chain #1.
XX
KW human; monoclonal antibody; phospholipase A2; PLA2;
KW inflammatory disorder; degenerative disorder;
KW joint inflammatory reaction; skin inflammatory reaction;
KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2004050850-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038234.
XX
PR 02-DEC-2002; 2002US-0430724P.
XX
PA (ARGE-) ARGENIX INC.
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI Jia X, Nocerini MR;
XX
DR WPI; 2004-461119/43.
XX
PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS Claim 1; SEQ ID NO 3; 128pp; English.
XX
CC The invention comprises a human monoclonal antibody that binds to
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC useful in the preparation of a medicament for the treatment of
CC inflammatory and degenerative disorders stemming from inflammatory
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC amino acid sequence represents the heavy chain from a monoclonal antibody
CC that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ Sequence 118 AA;
```

```
Alignment Scores:
Pred. No.: 0.0343 Length: 118
Score: 93.80 Matches: 19
Percent Similarity: 36.21% Conservative: 2
Best Local Similarity: 32.76% Mismatches: 5
Query Match: 63.38% Indels: 32
```

```
DB: 8 Gaps: 1
NOLAN463-2A.SEQ (1-84) x ADP47088 (1-118)
Qy 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAGGC--- 57
   |||||
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
   |||||
Qy 57 ----- 57
Db 70 IleSerAlaAspLysSerIleThrThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
Qy 58 -----AGTCAGGCTATTAGCAGCTGG 78
   |||||
Db 90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp 107
   |||||

Search completed: August 4, 2005, 18:55:54
Job time : 96 secs
```

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 CompuGen Ltd.
 OM nucleic - protein search, using frame_plus_n2p model
 Run on: August 4, 2005, 18:44:26 ; Search time 22.25 Seconds
 (without alignments)
 563.642 Million cell updates/sec

Title: NOLAN463-2A.SEQ
 Perfect score: 148
 Sequence: 1 ATCATCTATCTGCTGACTC.....GTATTAGCAGCTGGTTAGCC 84

Scoring table:
 BLOSUM62
 Xgapop 10.0 , Xgapext 0.1
 Ygapop 10.0 , Ygapext 0.1
 Fgapop 6.0 , Fgapext 0.1
 Delop 6.0 , Delext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+n2p.model -DEV=xlp
 -O=/cgn2_1/USPTO spool p/NOLAN08728463-2/runat_04082005 123945 22604/app_query.fasta_1.5
 -DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=NOLAN08728463-2 @CGN 1.1 66 @runat_04082005 123945 22604 -NCPU=6 -ICPU=3
 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
 -FGAEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Issued Patents AA:
 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
 5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep.*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 92.2 | 62.3 | 98 | 2 | US-08-665-202-33 |
| 2 | 92.2 | 62.3 | 98 | 4 | US-09-315-574-33 |
| 3 | 92.2 | 62.3 | 111 | 4 | US-09-726-219A-171 |
| 4 | 92.2 | 62.3 | 117 | 3 | US-08-545-809A-133 |
| 5 | 92.2 | 62.3 | 119 | 3 | US-09-025-769B-26 |
| 6 | 92.2 | 62.3 | 119 | 4 | US-09-490-070A-26 |
| 7 | 92.2 | 62.3 | 119 | 4 | US-09-490-153-26 |
| 8 | 92.2 | 62.3 | 119 | 4 | US-09-490-324-26 |
| 9 | 92.2 | 62.3 | 120 | 3 | US-09-025-769B-40 |
| 10 | 92.2 | 62.3 | 120 | 3 | US-09-025-769B-67 |
| 11 | 92.2 | 62.3 | 120 | 4 | US-09-490-070A-40 |
| 12 | 92.2 | 62.3 | 120 | 4 | US-09-490-070A-67 |

| | | | | | | |
|----|------|------|-----|---|-------------------|-------------------|
| 13 | 92.2 | 62.3 | 120 | 4 | US-09-490-153-40 | Sequence 40, Appl |
| 14 | 92.2 | 62.3 | 120 | 4 | US-09-490-153-67 | Sequence 67, Appl |
| 15 | 92.2 | 62.3 | 120 | 4 | US-09-490-324-40 | Sequence 40, Appl |
| 16 | 92.2 | 62.3 | 120 | 4 | US-09-490-324-67 | Sequence 67, Appl |
| 17 | 91.2 | 61.6 | 98 | 1 | US-08-478-039-81 | Sequence 81, Appl |
| 18 | 91.2 | 61.6 | 98 | 1 | US-08-478-349A-81 | Sequence 81, Appl |
| 19 | 91.2 | 61.6 | 125 | 2 | US-08-665-202-46 | Sequence 46, Appl |
| 20 | 91.2 | 61.6 | 125 | 2 | US-08-665-202-53 | Sequence 53, Appl |
| 21 | 91.2 | 61.6 | 125 | 2 | US-08-665-202-54 | Sequence 54, Appl |
| 22 | 91.2 | 61.6 | 125 | 2 | US-09-315-574-46 | Sequence 46, Appl |
| 23 | 91.2 | 61.6 | 125 | 4 | US-09-315-574-53 | Sequence 53, Appl |
| 24 | 91.2 | 61.6 | 125 | 4 | US-09-315-574-54 | Sequence 54, Appl |
| 25 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-44 | Sequence 44, Appl |
| 26 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-45 | Sequence 45, Appl |
| 27 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-47 | Sequence 47, Appl |
| 28 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-48 | Sequence 48, Appl |
| 29 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-49 | Sequence 49, Appl |
| 30 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-50 | Sequence 50, Appl |
| 31 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-51 | Sequence 51, Appl |
| 32 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-52 | Sequence 52, Appl |
| 33 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-55 | Sequence 55, Appl |
| 34 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-57 | Sequence 57, Appl |
| 35 | 88.4 | 59.7 | 125 | 2 | US-08-665-202-58 | Sequence 58, Appl |
| 36 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-44 | Sequence 44, Appl |
| 37 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-45 | Sequence 45, Appl |
| 38 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-47 | Sequence 47, Appl |
| 39 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-48 | Sequence 48, Appl |
| 40 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-49 | Sequence 49, Appl |
| 41 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-50 | Sequence 50, Appl |
| 42 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-51 | Sequence 51, Appl |
| 43 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-52 | Sequence 52, Appl |
| 44 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-55 | Sequence 55, Appl |
| 45 | 88.4 | 59.7 | 125 | 4 | US-09-315-574-57 | Sequence 57, Appl |

ALIGNMENTS

RESULT 1

US-08-665-202-33
 ; Sequence 33, Application US/08665202
 ; Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-33

Alignment Scores:
Pred. No.: 0.00843          Length: 98
Score: 92.20              Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30%      Indels: 8
DB: 2                      Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-08-665-202-33 (1-98)

Qy 1 ATCATCTATCTGGTGACTCTGATACCATACAGCCGCTCTTCCAAAGCGCG----- 54
Db 50 llllelyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 -----GCGAGTCACGGGTATTAGCAGC-----TGG 78
Db 70 llsSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 2
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-33

Alignment Scores:
Pred. No.: 0.00843          Length: 98
Score: 92.20              Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30%      Indels: 8
DB: 2                      Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-315-574-33 (1-98)

Qy 1 ATCATCTATCTGGTGACTCTGATACCATACAGCCGCTCTTCCAAAGCGCG----- 54
Db 50 llllelyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

Qy 55 -----GCGAGTCACGGGTATTAGCAGC-----TGG 78
Db 70 llsSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 3
US-09-726-219A-171
; Sequence 171, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 171
; LENGTH: 111
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-726-219A-171

Alignment Scores:
Pred. No.: 0.00879      Length: 111
Score: 92.20           Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-726-219A-171 (1-111)
QY 1 ATCATCTATCTGTCGACTCTGATACACATACAGCCGCTCTTCAAGCGCG----- 54
Db 50 IleleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69
QY 55 -----GCCAGTCAGGTTATTAGCAGC-----TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyLeuHisTrp 83

RESULT 4
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-133

Alignment Scores:
Pred. No.: 0.00895      Length: 117
Score: 92.20           Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 3 Gaps: 2

; ORGANISM: Homo sapiens
US-09-025-769B-26

Alignment Scores:
Pred. No.: 0.009      Length: 119
Score: 92.20           Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 3 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-025-769B-26 (1-119)
QY 1 ATCATCTATCTGTCGACTCTGATACACATACAGCCGCTCTTCAAGCGCG----- 54
Db 50 IleleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69
QY 55 -----GCCAGTCAGGTTATTAGCAGC-----TGG 78
Db 89 IleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 102

RESULT 5
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-26

Alignment Scores:
Pred. No.: 0.009      Length: 119
Score: 92.20           Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 3 Gaps: 2
```

Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 6
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

Alignment Scores:
Pred. No.: 0.009 Length: 119
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-070A-26 (1-119)

QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAAAGCGCG----- 54
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

QY 55 -----GCCAGTCAGGATTAGCAGC-----TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 7
US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Alignment Scores:
Pred. No.: 0.009 Length: 119
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-153-26 (1-119)

QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAAAGCGCG----- 54
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69

QY 55 -----GCCAGTCAGGATTAGCAGC-----TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 8
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming


```

; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
;
; INFORMATION FOR SEQ ID NO: 40:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 120 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: <Unknown>
;     TOPOLOGY: linear
;
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

Alignment Scores:
Pred. No.:          0.00902          Length:          120
Score:              92.20           Matches:         20
Percent Similarity: 67.65%          Conservative:      3
Best Local Similarity: 58.82%        Mismatches:       3
Query Match:        62.30%          Indels:           8
DB:                  4              Gaps:             2

NOLAN463-2A.SEQ (1-84) x US-09-490-070A-40 (1-120)
Qy      1  ATCATCTATCCTGGTACCTCTGATACCATACACAGCGCGTCTCTCAAGGCGG-----54
Db      50  IlellyrProGlyAspSerAspThrArgtyrSerProSerPheGlnGlyGlnValThr 69
Qy      55  -----GCGAGTCAGGATTATGACGAC-----TGG 78
Db      70  IleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTip 83

RESULT 12
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 696248
;
; GENERAL INFORMATION:
;   APPLICANT: Knappik, Achim
;               Pack, Peter
;               Ilag, Vic
;               Ge, Liming
;               Moroney, Simon
;               Plueckthun, Andreas
;
;   TITLE OF INVENTION: Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES: 373
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                 White & McAuliffe
;   STREET: 1666 K Street, N.W., Suite 300
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20006
;
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/490,070A
;     FILING DATE: 24-Jan-2000
;
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 95 11 3021.0
;     FILING DATE: 18-AUG-1995
;
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Colin G. Sandercock, Esq.
;     REGISTRATION NUMBER: 31,298
;     REFERENCE/DOCKET NUMBER: 37629-0005
;
;   TELECOMMUNICATION INFORMATION:

```



```

;
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Alignment Scores:
Pred. No.: 0.00902 Length: 120
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-070A-67 (1-120)
QY 1 ATCATCTATCTGGTGACTCTGATACCATACAGCCGCTCTCCAAAGCCGG----- 54
Db 50 llelletyProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr 69
QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 13
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid

```

```

;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

Alignment Scores:
Pred. No.: 0.00902 Length: 120
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-153-40 (1-120)
QY 1 ATCATCTATCTGGTGACTCTGATACCATACAGCCGCTCTCCAAAGCCGG----- 54
Db 50 llelletyProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyValThr 69
QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 14
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

```

Alignment Scores:
Pred. No.: 0.00902 Length: 120
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-09-490-153-67 (1-120)

QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAAAGCGCGG----- 54
|||||
Db 50 lilellyTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69
|||||
QY 55 -----GCGAGTCACGGGTATTAGCAGC-----TGG 78
|||||
Db 70 lileSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 83
|||||

RESULT 15
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40

Alignment Scores:
Pred. No.: 0.00902 Length: 120
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3

Query Match: 62.30% Indels: 8
DB: 4 Gaps: 2
NOLAN463-2A.SEQ (1-84) x US-09-490-324-40 (1-120)
QY 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCGCTCTTCCAAAGCGCGG----- 54
|||||
Db 50 lilellyTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69
|||||
QY 55 -----GCGAGTCACGGGTATTAGCAGC-----TGG 78
|||||
Db 70 lileSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 83
|||||

Search completed: August 4, 2005, 19:04:14
Job time : 25.25 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: August 4, 2005, 19:01:38 ; Search time 78.75 Seconds
(without alignments)
832.849 Million cell updates/sec

Title: NOLAN463-2A.SEQ
Perfect score: 148
Sequence: 1 ATCATCTATCTCGTGACTC.....GTATTAGCAGCTGGTTAGCC 84

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123947_22665/app_query.fasta_1.5
-DB=Published Applications AA -QWTF=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000
-USER=NOLAN08728463-2@cgn 1.1 260 @runat_04082005_123947_22665 -NCPU=6
-ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRA=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0 -DELOP=6 -DELEXT=0.1

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 97.9 | 66.1 | 116 | 10 | US-09-851-614-4 |
| 2 | 97.9 | 66.1 | 116 | 14 | US-10-035-637-4 |
| 3 | 97.9 | 66.1 | 116 | 16 | US-10-769-144-4 |
| 4 | 97.9 | 66.1 | 411 | 16 | US-10-769-144-12 |
| 5 | 97.9 | 66.1 | 468 | 16 | US-10-769-144-2 |
| 6 | 97.9 | 66.1 | 613 | 16 | US-10-769-144-10 |
| 7 | 96.2 | 65.0 | 118 | 17 | US-10-726-332-29 |
| 8 | 95.4 | 64.5 | 129 | 14 | US-10-041-860-29 |
| 9 | 95.4 | 64.5 | 129 | 14 | US-10-041-860-215 |
| 10 | 95.4 | 64.5 | 129 | 14 | US-10-041-860-250 |
| 11 | 95.4 | 64.5 | 129 | 16 | US-10-041-860-319 |
| 12 | 95.4 | 64.5 | 129 | 16 | US-10-665-383-38 |
| 13 | 94.9 | 64.1 | 116 | 17 | US-10-727-155-100 |
| 14 | 93.8 | 63.4 | 118 | 17 | US-10-726-332-3 |
| 15 | 93.5 | 63.2 | 118 | 17 | US-10-726-332-13 |
| 16 | 93.5 | 63.2 | 118 | 17 | US-10-726-332-139 |
| 17 | 93.5 | 63.2 | 118 | 17 | US-10-726-332-139 |
| 18 | 93.5 | 63.2 | 120 | 17 | US-10-638-265-62 |
| 19 | 93.5 | 63.2 | 120 | 17 | US-10-638-265-78 |
| 20 | 93.2 | 63.0 | 123 | 16 | US-10-466-242-49 |
| 21 | 93.2 | 63.0 | 301 | 14 | US-10-002-631C-114 |
| 22 | 92.4 | 62.4 | 225 | 16 | US-10-128-520-158 |
| 23 | 92.2 | 62.3 | 82 | 14 | US-10-078-958-5 |
| 24 | 92.2 | 62.3 | 98 | 14 | US-10-194-975-45 |
| 25 | 92.2 | 62.3 | 98 | 14 | US-10-125-687-16 |
| 26 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-6 |
| 27 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-301 |
| 28 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-302 |
| 29 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-312 |
| 30 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-314 |
| 31 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-318 |
| 32 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-320 |
| 33 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-336 |
| 34 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-338 |
| 35 | 92.2 | 62.3 | 98 | 14 | US-10-041-860-367 |
| 36 | 92.2 | 62.3 | 98 | 15 | US-10-308-817-88 |
| 37 | 92.2 | 62.3 | 98 | 15 | US-10-032-037B-106 |
| 38 | 92.2 | 62.3 | 98 | 15 | US-10-032-037B-108 |
| 39 | 92.2 | 62.3 | 98 | 15 | US-10-029-988B-106 |
| 40 | 92.2 | 62.3 | 98 | 15 | US-10-029-988B-108 |
| 41 | 92.2 | 62.3 | 98 | 15 | US-10-032-423A-106 |
| 42 | 92.2 | 62.3 | 98 | 15 | US-10-032-423A-108 |
| 43 | 92.2 | 62.3 | 98 | 15 | US-10-453-698-88 |
| 44 | 92.2 | 62.3 | 98 | 15 | US-10-029-926B-106 |
| 45 | 92.2 | 62.3 | 98 | 15 | US-10-029-926B-108 |

ALIGNMENTS

RESULT 1
US-09-851-614-4
; Sequence 4, Application US/09851614
; Publication No. US20030167502A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keller, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; ; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166
; CURRENT APPLICATION NUMBER: US/09/851,614
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

```
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-614-4

Alignment Scores:
Pred. No.:          0.0173      Length: 116
Score:             97.90      Matches: 19
Percent Similarity: 36.84%    Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match:       66.15%     Indels: 31
DB:               10         Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-09-851-614-4 (1-116)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCGCTCTTCCAAGGC----- 51
Db 50 llelleTyProGlyAspSerAspThrIleTySerProSerPheGlnGlyValThr 69
QY 51 ----- 51
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGGCGAGTCAGGTATTAGCAGCTGG 78
Db 90 AspThrAlaMetTyTyTyCysThrArgGlyAspArgGlyValAspTyTrp 106

RESULT 2
US-10-035-637-4
; Sequence 4, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-035-637-4

Alignment Scores:
Pred. No.:          0.0173      Length: 116
Score:             97.90      Matches: 19
Percent Similarity: 36.84%    Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match:       66.15%     Indels: 31
DB:               14         Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-035-637-4 (1-116)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCGCTCTTCCAAGGC----- 51
Db 50 llelleTyProGlyAspSerAspThrIleTySerProSerPheGlnGlyValThr 69
QY 51 ----- 51
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGGCGAGTCAGGTATTAGCAGCTGG 78
Db 90 AspThrAlaMetTyTyTyCysThrArgGlyAspArgGlyValAspTyTrp 106

RESULT 3
US-10-769-144-4
; Sequence 4, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-4

Alignment Scores:
Pred. No.:          0.0173      Length: 116
Score:             97.90      Matches: 19
Percent Similarity: 36.84%    Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match:       66.15%     Indels: 31
DB:               16         Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-4 (1-116)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCGCTCTTCCAAGGC----- 51
Db 50 llelleTyProGlyAspSerAspThrIleTySerProSerPheGlnGlyValThr 69
QY 51 ----- 51
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGGCGAGTCAGGTATTAGCAGCTGG 78
Db 90 AspThrAlaMetTyTyTyCysThrArgGlyAspArgGlyValAspTyTrp 106

RESULT 4
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Alignment Scores:
Pred. No.:          0.0173      Length: 116
Score:             97.90      Matches: 19
Percent Similarity: 36.84%    Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match:       66.15%     Indels: 31
DB:               14         Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-035-637-4 (1-116)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCGCTCTTCCAAGGC----- 51
Db 50 llelleTyProGlyAspSerAspThrIleTySerProSerPheGlnGlyValThr 69
QY 51 ----- 51
Db 70 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGGCGAGTCAGGTATTAGCAGCTGG 78
```

```
Pred. No.: 0.0236 Length: 411
Score: 97.90 Matches: 19
Percent Similarity: 36.84% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 66.15% Indels: 31
DB: 16 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-12 (1-411)

QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAAAGC----- 51
Db 191 lleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 210
QY 51 ----- 51
Db 211 lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 230
QY 52 -----CGGCGCAGTCAGGCTATTAGCAGCTGG 78
Db 231 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 247

RESULT 5
US-10-769-144-2
; Sequence 2, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-2

Alignment Scores:
Pred. No.: 0.0244 Length: 468
Score: 97.90 Matches: 19
Percent Similarity: 36.84% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 66.15% Indels: 31
DB: 16 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-2 (1-468)

QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAAAGC----- 51
Db 69 lleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88
QY 51 ----- 51
Db 89 lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
QY 52 -----CGGCGCAGTCAGGCTATTAGCAGCTGG 78
Db 109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125

RESULT 6
US-10-769-144-10
; Sequence 10, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MXI-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-10

Alignment Scores:
Pred. No.: 0.0236 Length: 613
Score: 97.90 Matches: 19
Percent Similarity: 36.84% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 66.15% Indels: 31
DB: 16 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-769-144-10 (1-613)

QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAAAGC----- 51
Db 69 lleIleTyrProGlyAspSerAspThrIleTyrSerProSerPheGlnGlyGlnValThr 88
QY 51 ----- 51
Db 89 lleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 108
QY 52 -----CGGCGCAGTCAGGCTATTAGCAGCTGG 78
Db 109 AspThrAlaMetTyrTyrCysThrArgGlyAspArgGlyValAspTyrTrp 125

RESULT 7
US-10-726-332-29
; Sequence 29, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-29

Alignment Scores:
Pred. No.: 0.0275 Length: 118
Score: 96.20 Matches: 21
Percent Similarity: 67.65% Conservative: 2
Best Local Similarity: 61.76% Mismatches: 3
```

```
Query Match: 65.00% Indels: 8
DB: 17 Gaps: 2
NOLAN463-2A.SEQ (1-84) x US-10-726-332-29 (1-118)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 55 -----GGAGTTCAGGGTATTAGCAGC-----TGG 78
Db 70 lileSerAlaAspGlnSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 8
US-10-041-860-29
; Sequence 29, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-29
Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservatve: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1
NOLAN463-2A.SEQ (1-84) x US-10-041-860-29 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 61 CAGGGTATTAGCAGC-----TGG 78
Db 70 -----lileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 9
US-10-041-860-215
; Sequence 215, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-250
Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservatve: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1
NOLAN463-2A.SEQ (1-84) x US-10-041-860-29 (1-118)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 61 CAGGGTATTAGCAGC-----TGG 78
Db 70 -----lileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 10
US-10-041-860-250
; Sequence 250, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-250
Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservatve: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1
NOLAN463-2A.SEQ (1-84) x US-10-041-860-250 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 61 CAGGGTATTAGCAGC-----TGG 78
Db 70 -----lileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 11
```

```
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-215
Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservatve: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1
NOLAN463-2A.SEQ (1-84) x US-10-041-860-215 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 61 CAGGGTATTAGCAGC-----TGG 78
Db 70 -----lileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 10
US-10-041-860-250
; Sequence 250, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-250
Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservatve: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1
NOLAN463-2A.SEQ (1-84) x US-10-041-860-250 (1-129)
QY 1 ATCATCTATCTGGTGACTCTGTATACCATACAGCCGCTCTTCCAAAGCGCGGAGT 60
Db 50 lilellyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 61 CAGGGTATTAGCAGC-----TGG 78
Db 70 -----lileSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83
RESULT 11
```

```
US-10-041-860-319
; Sequence 319, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-319

Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 64.46% Indels: 16
DB: 14 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-041-860-319 (1-129)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAGGCGGGCGAGT 60
Db 50 lleiletyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyAlaThr 69
QY 61 CAGGTATTAGCAGC-----TGG 78
Db 70 -----lleSerAlaAspLysSerIleThrAlaTyrLeuGlnTrp 83

RESULT 12
US-10-665-383-38
; Sequence 38, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-38

Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 1

US-10-041-860-319
; Sequence 319, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-319

Alignment Scores:
Pred. No.: 0.0348 Length: 129
Score: 95.40 Matches: 20
Percent Similarity: 57.50% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 1

NOLAN463-2A.SEQ (1-84) x US-10-041-860-319 (1-129)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAGGCGGGCGAGT 60
Db 50 lleiletyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyAlaThr 69
QY 61 CAGGTATTAGCAGC-----TGG 78
Db 70 -----lleSerAlaAspLysSerIleThrAlaTyrLeuGlnTrp 83

RESULT 13
US-10-727-155-100
; Sequence 100, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaapal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raifaela Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-100

Alignment Scores:
Pred. No.: 0.0388 Length: 116
Score: 94.90 Matches: 19
Percent Similarity: 36.84% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 5
Query Match: 64.12% Indels: 31
DB: 17 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-727-155-100 (1-116)
QY 1 ATCATCTATCTGGTACTCTGATACCATACAGCCCGTCTTCCAGGCGGGCGAGT 51
Db 50 lleiletyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyAlaThr 69
QY 51 -----TGG 78
Db 70 -----lleSerAlaAspLysSerIleThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
QY 52 -----CGGCGGAGTCAGGGTATTAGCAGTGG 78
Db 90 AspThrAlaMetTyrTyrCysAlaArgSerGlyTyrGlyMetAspValTrp 106

RESULT 14
US-10-726-332-3
; Sequence 3, Application US/10726332
```

; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726.332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-3

Alignment Scores:
Pred. No.: 0.0523 Length: 118
Score: 93.80 Matches: 19
Percent Similarity: 36.21% Conservative: 2
Best Local Similarity: 32.76% Mismatches: 5
Query Match: 63.38% Indels: 32
DB: 17 Gaps: 1

NOLAN463-2A.SEQ (1-84) x US-10-726-332-3 (1-118)

```
Qy 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCCGCTCTCCAGGCGGCGG--- 57
Db 50 llelleTyPrGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
Qy 57 -----AGTCAGGCTATTACGAGCTGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
Qy 58 -----AGTCAGGCTATTACGAGCTGG 78
Db 90 AspThrAlaMetTyrTyrCysAlaArgHisTrpSerTyrGlyMetAspValTrp 107
```

RESULT 15

US-10-726-332-5
; Sequence 5, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726.332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-726-332-5

Alignment Scores:
Pred. No.: 0.0567 Length: 118
Score: 93.50 Matches: 21
Percent Similarity: 45.10% Conservative: 2
Best Local Similarity: 41.18% Mismatches: 3
Query Match: 63.18% Indels: 25
DB: 17 Gaps: 2

NOLAN463-2A.SEQ (1-84) x US-10-726-332-5 (1-118)

```
Qy 1 ATCATCTATCTGGTGACTCTGATACACATACAGCCCGCTCTCCAGGCGGCGG--- 54
Db 50 llelleTyPrGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
Qy 55 -----GCCGAGTCAGGCTATTAGC----- 72
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
Qy 73 -----AGCTGG 78
Db 90 AspThrAlaMetTyrTyrCysAlaArgSerTrp 100
```

Search completed: August 4, 2005, 19:30:17
Job time : 80.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:42:17 ; Search time 17.75 Seconds
(without alignments)
910.671 Million cell updates/sec

Title: NOLAN463-2A.SEQ
Perfect score: 148
Sequence: 1 ATCATCTATCTGCTGACTC.....GTATTAGCAGCTGGTTAGCC 84

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool_p/NOLAN08728463-2/runat_04082005_123944_22592/app_query.fasta_1.5
-DB=PIR -OPWT=fastan -SUFFIX=rxp -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THRM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN08728463-2 @CGN 1.1 77 @runat_04082005_123944_22592 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | |
|------------|-------|-------------|--------|----|-------------|--------------------|
| Result No. | Score | Query Match | Length | ID | Description | |
| 1 | 95.6 | 64.6 | 102 | 2 | PH1281 | Ig heavy chain V r |
| 2 | 95.6 | 64.6 | 102 | 2 | PH1249 | Ig heavy chain V r |
| 3 | 93.3 | 63.0 | 127 | 2 | PH1409 | Ig heavy chain V r |
| 4 | 93.2 | 63.0 | 127 | 2 | PH1414 | Ig heavy chain V r |
| 5 | 92.4 | 62.6 | 123 | 2 | PH3606 | Ig heavy chain V r |
| 6 | 92.4 | 62.4 | 98 | 2 | PH0877 | Ig heavy chain V r |
| 7 | 92.2 | 62.3 | 98 | 2 | PH1274 | Ig heavy chain V r |
| 8 | 92.2 | 62.3 | 98 | 2 | S26907 | Ig heavy chain V r |
| 9 | 92.2 | 62.3 | 101 | 2 | S12424 | Ig heavy chain V r |
| 10 | 92.2 | 62.3 | 102 | 2 | PH1266 | Ig heavy chain V r |
| 11 | 92.2 | 62.3 | 102 | 2 | PH1279 | Ig heavy chain V r |
| 12 | 92.2 | 62.3 | 102 | 2 | PH1277 | Ig heavy chain V r |
| 13 | 92.2 | 62.3 | 102 | 2 | PH1244 | Ig heavy chain V r |
| 14 | 92.2 | 62.3 | 102 | 2 | PH1272 | Ig heavy chain V r |

| | | | | | | |
|----|------|------|-----|---|--------|--------------------|
| 15 | 92.2 | 62.3 | 102 | 2 | PH1282 | Ig heavy chain V r |
| 16 | 92.2 | 62.3 | 102 | 2 | PH1248 | Ig heavy chain V r |
| 17 | 92.2 | 62.3 | 102 | 2 | PH1280 | Ig heavy chain V r |
| 18 | 92.2 | 62.3 | 102 | 2 | PH1258 | Ig heavy chain V r |
| 19 | 92.2 | 62.3 | 102 | 2 | PH1264 | Ig heavy chain V r |
| 20 | 92.2 | 62.3 | 102 | 2 | PH1273 | Ig heavy chain V r |
| 21 | 92.2 | 62.3 | 102 | 2 | PH1271 | Ig heavy chain V r |
| 22 | 92.2 | 62.3 | 102 | 2 | PH1278 | Ig heavy chain V r |
| 23 | 92.2 | 62.3 | 104 | 2 | B36006 | Ig heavy chain V r |
| 24 | 92.2 | 62.3 | 113 | 2 | PH1428 | Ig heavy chain V r |
| 25 | 92.2 | 62.3 | 115 | 2 | PH1557 | Ig heavy chain V r |
| 26 | 92.2 | 62.3 | 117 | 2 | A28846 | Ig heavy chain pre |
| 27 | 92.2 | 62.3 | 117 | 2 | PH1670 | Ig heavy chain V r |
| 28 | 92.2 | 62.3 | 123 | 2 | PH1423 | Ig heavy chain V r |
| 29 | 92.2 | 62.3 | 123 | 2 | S38492 | Ig heavy chain - h |
| 30 | 92.2 | 62.3 | 127 | 2 | PH1411 | Ig heavy chain V r |
| 31 | 92.2 | 62.3 | 128 | 2 | S16685 | Ig heavy chain V r |
| 32 | 92.2 | 62.3 | 136 | 2 | A49047 | Ig heavy chain V r |
| 33 | 92.2 | 62.3 | 136 | 2 | PH1559 | Ig heavy chain V r |
| 34 | 92.2 | 62.3 | 139 | 2 | PH1558 | Ig heavy chain V r |
| 35 | 91.4 | 61.8 | 101 | 2 | S12428 | Ig heavy chain V r |
| 36 | 90.4 | 61.1 | 102 | 2 | PH1267 | Ig heavy chain V r |
| 37 | 90.4 | 61.1 | 102 | 2 | PH1259 | Ig heavy chain V r |
| 38 | 90.4 | 61.1 | 134 | 2 | PH1422 | Ig heavy chain V r |
| 39 | 90.2 | 60.9 | 119 | 2 | S36257 | Ig heavy chain V r |
| 40 | 89.6 | 60.5 | 127 | 2 | PH1420 | Ig heavy chain V r |
| 41 | 89.2 | 60.3 | 102 | 2 | PH1252 | Ig heavy chain V r |
| 42 | 88.4 | 59.7 | 123 | 2 | PH1413 | Ig heavy chain V r |
| 43 | 88.2 | 59.6 | 102 | 2 | PH1247 | Ig heavy chain V r |
| 44 | 87.2 | 58.9 | 86 | 2 | S12580 | Ig heavy chain V r |
| 45 | 87.2 | 58.9 | 102 | 2 | PH1265 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1281
R:Car, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A>Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1281
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
P:19-103/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00273 Length: 102
Score: 95.60 Matches: 19
Percent Similarity: 77.78% Conservative: 2
Best Local Similarity: 70.37% Mismatches: 2
Query Match: 64.59% Indels: 4
DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x PH1281 (1-102)

Qy 1 ATCATCTATCTGCTGACTCTGATACCATACAGCCGCTCTTCCAGGCGGCGGAGT 60

Db 54 lIlelleYrProGlyAspSerAspThrArgTyrSerProSerPheGln----GlyGlnVa 72

Qy 61 CAGGCTATTAGCA 73

Db 72 lThrIleleuAla 76

RESULT 2

PH1249

Ig heavy chain V region (clone CORD7) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1249

R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chronic dermatitis.

A:Reference number: PH1232; MUID:93018922; PMID:1402653

A:Accession: PH1249

A:Molecule type: DNA

A:Residues: 1-102 <CAI>

A:Experimental source: cord blood B cell

A>Note: the authors translated the stop codon for residue 5 as X

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00273 Length: 102
Score: 95.60 Matches: 19
Percent Similarity: 77.78% Conservative: 2
Best Local Similarity: 70.37% Mismatches: 2
Query Match: 64.59% Indels: 4
DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x PH1249 (1-102)

Qy 1 ATCATCTATCTGGTGACTCTGATACACATACACCGCGTCTTCCAAAGCGCGGCGAGT 60

|||||
Db 54 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnVa 72

|||||

Qy 61 CAGGTATTAGCA 73

|||||

Db 72 lThrIleuAla 76

|||||

RESULT 3

PH1409

Ig heavy chain V region (clone P1-51) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1409

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of E dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1409

A:Molecule type: mRNA

A:Residues: 1-127 <VAN>

A:Experimental source: PBMC

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00533 Length: 127
Score: 93.30 Matches: 18
Percent Similarity: 70.00% Conservative: 3
Best Local Similarity: 60.00% Mismatches: 2
Query Match: 63.04% Indels: 7
DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x PH1409 (1-127)

Qy 1 ATCATCTATCTGGTGACTCTGATACACATACACCGCGTCTTCCAAAGCGCGGCGAGT 60

|||||

Db 50 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyArgValThr 69

|||||

Qy 61 CAGGTATTAGCAGT 76

|||||

Db 70 -----MetSerAla 72

|||||

RESULT 4

PH1414

Ig heavy chain V region (clone P1-54) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1414

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of E dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1414

A:Molecule type: mRNA

A:Residues: 1-127 <VAN>

A:Experimental source: PBMC

A>Note: the authors translated the codon TTG for residue 119 as Met

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00548 Length: 127
Score: 93.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.97% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1414 (1-127)

Qy 1 ATCATCTATCTGGTGACTCTGATACACATACACCGCGTCTTCCAAAGCGCGG----- 54

|||||

Db 50 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69

|||||

Qy 55 -----GCGAGTCACGGGTATTAGCAGC-----TCG 78

|||||

Db 70 lIleSerAlaAspGluSerIleSerThrAlaTyLeuGlnTrp 83

|||||

RESULT 5

C36006

Ig heavy chain V region (83p2) - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C:Accession: C36006

R:Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A:Reference number: A36005; MUID:90349571; PMID:2117273

A:Accession: C36006

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <SCH>

A:Cross-references: GB:M34022

C:Genetics:

A:Gene: GDB:IGH@; IGHDY1

A:Cross-references: GDB:118731; OMIM:146910

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00632 Length: 123
Score: 92.70 Matches: 19
Percent Similarity: 35.59% Conservative: 2
Best Local Similarity: 32.20% Mismatches: 5
Query Match: 62.64% Indels: 33
DB: 2 Gaps: 1

NOLAN463-2A.SEQ (1-84) x C36006 (1-123)

Qy 1 ATCATCTATCTGGTGACTCTGATACACATACACCGCGTCTTCCAAAGCGCGG----- 54

|||||

Db 50 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 69

|||||

```
QY 54 ----- 54
Db 70 IleSerAlaAspLysSerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSer 89
QY 55 -----GCAGTCACGGTATTAGCAGCTGG 78
Db 90 AspThrAlaMetTyrTyrCysAlaArgHisAsnSerGlnThrGlyAlaSerLeuTrp 108

RESULT 6
PH0877
Ig heavy chain V region (anti-DNA, II-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C:Accession: PH0877
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0877
A:Molecule type: DNA
A:Residues: 1-98 <MAN>
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2

Alignment Scores:
Pred. No.: 0.00682 Length: 98
Score: 92.40 Matches: 18
Percent Similarity: 56.41% Conservative: 4
Best Local Similarity: 46.15% Mismatches: 1
Query Match: 62.43% Indels: 16
DB: 2 Gaps: 1

NOLAN463-2A.SEQ (1-84) x PH0877 (1-98)
QY 4 ATCTATCTCTGGTACTCTGATACCATACAGCCGCTCTTCCAAAGCGCGGAGTCAG 63
Db 51 ValTyrProGlyAspSerAspThrTyrSerProSerPheGlnGlyGlnValThr 69
QY 64 GGTATTAGCAGC-----TGG 78
Db 70 ---IleSerAlaAspLysCysIleSerThrAlaTyrLeuGlnTrp 83

RESULT 7
PH1274
Ig heavy chain V region (clone PBL5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1274
R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1274
A:Molecule type: DNA
A:Residues: 1-98 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 0.00722 Length: 98
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1274 (1-98)
```

```
QY 1 ATCATCTATCTCTGGTACTCTGATACCATACAGCCGCTCTTCCAAAGCGCGG----- 54
Db 54 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 73
QY 55 -----GCAGTCACGGTATTAGCAGC-----TGG 78
Db 74 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 87

RESULT 8
S26907
Ig heavy chain V region (DP-73) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26907
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26907
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12373; NID:G32965; PIDN:CAA78243.1; PID:G32966
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00722 Length: 98
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x S26907 (1-98)
QY 1 ATCATCTATCTCTGGTACTCTGATACCATACAGCCGCTCTTCCAAAGCGCGG----- 54
Db 50 IleIleTyrProGlyAspSerAspThrArgTyrSerProSerPheGlnGlyGlnValThr 69
QY 55 -----GCAGTCACGGTATTAGCAGC-----TGG 78
Db 70 IleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 83

RESULT 9
S12424
Ig heavy chain V region (5) - human
C:Species: Homo sapiens (man)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 03-Aug-1998
C:Accession: S12424; S12425; S12426; S12427; S12429; S12432
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12424
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SAN>
A:Cross-references: EMBL:X56372
A:Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
A:Accession: S12425
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SA2>
A:Cross-references: EMBL:X56373
A:Accession: S12426
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SAJ>
A:Cross-references: EMBL:X56370
A:Accession: S12427
```

A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SA4>
A:Cross-references: EMBL:X56368
A:Accession: S12429
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SA5>
A:Cross-references: EMBL:X56369
A:Accession: S12432
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <SA6>
A:Cross-references: EMBL:X56371
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:18-101/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00723 Length: 101
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x S12424 (1-101)

QY 1 ATCATCTATCTCGTGACTCTGATACCATACAGCCGCTCTTCCAGGCGG----- 54

Db 53 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 72

QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78

Db 73 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 86

RESULT 10

PH1266

Ig heavy chain V region (clone VERGS) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1266
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1266
A:Molecule type: mRNA
A:Residues: 1-102 <CAI>
A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00723 Length: 102
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1266 (1-102)

QY 1 ATCATCTATCTCGTGACTCTGATACCATACAGCCGCTCTTCCAGGCGG----- 54

Db 54 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 73

QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78

Db 74 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 87

RESULT 11

PH1244

PH1279

Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD-
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1279
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1279
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00723 Length: 102
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1279 (1-102)

QY 1 ATCATCTATCTCGTGACTCTGATACCATACAGCCGCTCTTCCAGGCGG----- 54

Db 54 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 73

QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78

Db 74 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 87

RESULT 12

PH1277

Ig heavy chain V region (clone PBL8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1277
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1277
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00723 Length: 102
Score: 92.20 Matches: 20
Percent Similarity: 67.65% Conservative: 3
Best Local Similarity: 58.82% Mismatches: 3
Query Match: 62.30% Indels: 8
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x PH1277 (1-102)

QY 1 ATCATCTATCTCGTGACTCTGATACCATACAGCCGCTCTTCCAGGCGG----- 54

Db 54 llelleTyProGlyAspSerAspThrArgTySerProSerPheGlnGlyGlnValThr 73

QY 55 -----GCGAGTCAGGGTATTAGCAGC-----TGG 78

Db 74 lleSerAlaAspLysSerIleSerThrAlaTyLeuGlnTrp 87

RESULT 13

PH1244

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1282
R;Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A;Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro-
A;Reference number: PH1232; MUID:93018822; PMID:1402653
A;Accession: PH1282
A;Molecule type: DNA
A;Residues: 1-102 <CAI>
A;Experimental source: adult PBL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```

Alignment Scores:
Pred. No.:      0.00723      Length:      102
Score:          92.20       Matches:      20
Percent Similarity: 67.65%   Conservative: 3
Best Local Similarity: 58.82% Mismatches:      3
Query Match:     62.30%     Indels:       8
DB:              2         Gaps:         2

NOLAN463-2A.SEQ (i-84) x PH1282 (1-102)

Qy      1  ATCATCTATCTCGTGACTCTGATACCACATACAGCCGCTCTTCCAGGCCGG----- 54
          |||||
Db      54  IleIeTyTProGlyAspSerAspThrArgTyTSerProSerPheGlnGlyGlnValThr 73
          |||||

Qy      55  -----GCCAGTTCAGGGTATTACGACG-----TGG 78
          |||  ::|  |||||::|
Db      74  IleSerAlaAspIysSerIleSerThrThrTyTLeuGlnTirp 87
          |||  ::|  |||||

```

Search completed: August 4, 2005, 19:02:36
Job time : 18.75 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 CompuGen Ltd.
 OM nucleic - protein search, using frame_plus_n2p model
 Run on: August 4, 2005, 18:23:15 ; Search time 80.75 Seconds
 (without alignments)
 1065.378 Million cell updates/sec

Title: NOLAN463-2A.SEQ
 Perfect score: 148
 Sequence: 1 ARCATCTATCTCTGTGACTC.....GTATTAGCAGCTGTTAGCC 84

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.1
 Ygapop 10.0 , Ygapext 0.1
 Fgapop 6.0 , Fgapext 0.1
 Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
 -MODEL=frame+n2p.model -DEV=xlp
 -Q=/cqn2.1/USPTO.spool.p/NOLAN08728463-2/runat_04082005_123944_23581/app_query.fasta_1.5
 -DB=Uniprot -QFWT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THRM SCORES=0 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=NOLAN08728463-2 @CGN 1.1 305 @runat_04082005_123944_23581 -NCPU=6
 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DSELEXT=0.1

Database : Uniprot 03.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|---------------------|
| 1 | 70.3 | 47.5 | 118 | Q921C4 | Q921C4 mus musculus |
| 2 | 68.3 | 46.1 | 111 | Q9D9B8 | Q9D9B8 mus musculus |
| 3 | 68.3 | 46.1 | 474 | Q8R3H6 | Q8R3H6 mus musculus |
| 4 | 67.6 | 45.7 | 236 | Q6GMX8 | Q6GMX8 homo sapien |
| 5 | 67.3 | 45.5 | 614 | Q7TMT6 | Q7TMT6 mus musculus |
| 6 | 64.4 | 42.4 | 302 | Q9I9C3 | Q9I9C3 anguilla an |
| 7 | 63.6 | 43.0 | 117 | KV11 HUMAN | P01601 homo sapien |
| 8 | 63.6 | 43.0 | 236 | Q6PIH7 | Q6PIH7 homo sapien |
| 9 | 63.5 | 42.9 | 474 | Q7Q1B6 | Q7Q1B6 anopheles g |
| 10 | 62.3 | 42.1 | 117 | HV52 MOUSE | P06327 mus musculus |
| 11 | 62.2 | 42.0 | 436 | Q6TL49 | Q6TL49 glyceria fl |
| 12 | 62 | 40.8 | 138 | Q72WG5 | Q72WG5 desulfovibr |
| C 13 | 61.8 | 40.7 | 984 | Q8MT62 | Q8MT62 drosophila |
| C 14 | 61.8 | 40.7 | 1043 | Q9YVS8 | Q9YVS8 drosophila |
| C 15 | 61.8 | 40.7 | 1059 | Q76NS2 | Q76NS2 drosophila |
| C 16 | 61.7 | 40.6 | 427 | Q9AYR4 | Q9AYR4 chaetoceros |

| | | | | | | |
|------|------|------|-----|---|------------|---------------------|
| C 17 | 61.7 | 40.6 | 427 | 2 | Q9AYR6 | Q9AYR6 chaetoceros |
| 18 | 61.3 | 41.4 | 110 | 2 | Q9JL83 | Q9JL83 mus musculus |
| 19 | 61 | 41.2 | 117 | 1 | HV06 MOUSE | P01750 mus musculus |
| 20 | 60.8 | 41.1 | 293 | 2 | Q73WB2 | Q73WB2 mycobacteri |
| 21 | 60.6 | 40.9 | 324 | 2 | Q7V9E2 | Q7V9E2 prochloroco |
| C 22 | 60.5 | 39.8 | 517 | 2 | Q9Y781 | Q9Y781 coprinus ci |
| C 23 | 60.3 | 39.7 | 660 | 1 | YG39_PSESM | Q8860 pseudomonas |
| C 24 | 60 | 39.5 | 609 | 2 | Q9ARZ1 | Q9ARZ1 oryza sativ |
| C 25 | 60 | 39.5 | 624 | 2 | Q9FMN8 | Q9FMN8 arabidopsis |
| C 26 | 60 | 39.5 | 929 | 2 | Q7F8S7 | Q7F8S7 oryza sativ |
| 27 | 59.9 | 40.5 | 240 | 2 | Q7PKV0 | Q7PKV0 anopheles g |
| 28 | 59.9 | 40.5 | 882 | 2 | Q7EUM0 | Q7EUM0 anopheles g |
| 29 | 59.9 | 40.5 | 930 | 2 | Q7PY03 | Q7PY03 anopheles g |
| 30 | 59.8 | 40.4 | 244 | 2 | Q65ZC8 | Q65ZC8 homo sapien |
| C 31 | 59.8 | 39.3 | 270 | 1 | VMT1_DHV11 | Q01479 dhori virus |
| C 32 | 59.7 | 39.3 | 189 | 2 | Q6ZR89 | Q6ZR89 homo sapien |
| 33 | 59.7 | 40.3 | 354 | 2 | Q27328 | Q27328 methanobact |
| 34 | 59.6 | 40.3 | 323 | 2 | Q8LDS8 | Q8LDS8 arabidopsis |
| 35 | 59.6 | 40.3 | 323 | 2 | Q94909 | Q94909 arabidopsis |
| 36 | 59.6 | 40.3 | 353 | 2 | Q9LFW2 | Q9LFW2 arabidopsis |
| 37 | 59.3 | 40.1 | 481 | 2 | Q91WT1 | Q91WT1 mus musculus |
| 38 | 59.3 | 40.1 | 724 | 2 | Q41384 | Q41384 spinacia ol |
| 39 | 59 | 39.9 | 460 | 2 | Q66IF9 | Q66IF9 xenopus tro |
| 40 | 58.8 | 39.7 | 161 | 2 | Q6JH66 | Q6JH66 ambystoma t |
| 41 | 58.7 | 39.7 | 596 | 2 | Q74C03 | Q74C03 geobacter s |
| 42 | 58.7 | 39.7 | 777 | 2 | Q6EP64 | Q6EP64 oryza sativ |
| 43 | 58.7 | 39.7 | 793 | 2 | Q7QXY1 | Q7QXY1 giardia lam |
| 44 | 58.6 | 39.6 | 117 | 1 | KV1J HUMAN | P01602 homo sapien |
| 45 | 58.4 | 39.5 | 477 | 2 | Q89HML | Q89HML bradyrhizob |

ALIGNMENTS

RESULT 1
 Q921C4 PRELIMINARY; PRT: 118 AA.
 ID Q921C4;
 AC Q921C4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.A., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells.";
 RL Mol. Immunol. 34:441-452(1997).
 DR EMBL; U78801; AAD00293.1; -;
 DR HSSP; P01751; INQB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON TER 1
 FT NON TER 118
 SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Alignment Scores:
 Pred. No.: 12.1 Length: 118
 Score: 70.30 Matches: 13
 Percent Similarity: 62.07% Conservative: 5
 Best Local Similarity: 44.83% Mismatches: 4
 Query Match: 47.50% Indels: 7
 DB: 2 Gaps: 0

| | |
|---|--|
| RA | Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., |
| RA | Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., |
| RA | Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., |
| RA | Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., |
| RA | Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M., |
| RA | Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., |
| RA | Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., |
| RA | Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., |
| RA | Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., |
| RA | Tsurumatsu M., Hayashizaki Y., |
| RL | Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. |
| DR | EMBL; AK007163; BAB24877.1; -- |
| DR | HSSP; P01820; IG7U. |
| DR | InterPro; IPR007110; Ig-like. |
| DR | InterPro; IPR003596; IG_V. |
| DR | SMART; SM00406; IGV; 1. |
| DR | PROSITE; PS50835; IG_LIKE; 1. |
| DR | SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64; |
| SD | |
| Alignment Scores: | |
| Pred. No.: | 21.5 |
| Score: | 68.30 |
| Percent Similarity: | 58.62% |
| Best Local Similarity: | 44.83% |
| Query Match: | 46.15% |
| Indels: | 7 |
| Gaps: | 0 |
| Length: 111 | |
| Matches: 13 | |
| Conservative: 4 | |
| Mismatches: 5 | |
| Indels: 7 | |
| Gaps: 0 | |
| NOTAN463-2A.SEQ (1-84) x Q9D9B8 (1-111) | |
| Qy | 4 ATCTATCTGGTGACTCTCATACCACTACAGCCCGTCCTTCCAAAGCGGCGGAGTCAG 63 |
| Dd | 57 Ilety-ProgIlyAspGlyAspThrAsnTyAsnGlyLySPhLeYsAlathr--- 75 |
| Qy | 64 GGTATTAGCAGCT 76 |
| Dd | 76 ----LeuThrAla 78 |
| RESULT 3 | |
| Q8R3H6 | PRELIMINARY; PRT; 474 AA. |
| AC | Q8R3H6; |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Created) |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) |
| DT | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) |
| DE | AU044919 protein. |
| GN | Name=AU044919; |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | SEQUENCE FROM NA. |
| RC | STRAIN=CZECH II; TISSUE=Mammary tumor; |
| RX | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., |
| RA | Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., |
| RA | Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carancini P., Prange C., |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., |
| RA | Boas A.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., |
| RA | Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A., |
| RA | Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., |
| RA | Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E., |
| RA | Jones S.J., Marra M.A.; |
| RT | "Generation and initial analysis of more than 15,000 full-length human |
| RT | and mouse cDNA sequences." |

RT and mouse cDNA sequences.["];
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBIJ databases.
DR EMBL; BC073764; AAH73764.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG.LIKE; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BFC9 CRC64;

Alignment Scores:
Pred. No.: 29.7 Length: 236
Score: 67.60 Matches: 18
Percent Similarity: 47.50% Conservative: 1
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 45.68% Indels: 14
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x Q6GMX8 (1-236)
Qy 7 TATCTCGGT-----GACTCTGATACCACATAGCCCGTCC----- 42
Db 17 PheProGlySerArgCysAspIleGlnMetThrGlnSerProSerValSerAlaSer 36
Qy 43 -----TTCCAAGCCGGCGGCGAGTCAGGGGTATTAGCAGCTGGTTAGCC 84
Db 37 ValGlyAspArgValThrIleThrCysArgAlaSerGlnGlyLeSerTerTrpLeuAla 56

RESULT 5
Q7TWT6 PRELIMINARY; PRT; 614 AA.

ID Q7TWT6
AC Q7TWT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/GNCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marushka K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettenan M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skalske J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Grimalkin J., Smallick D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marxa M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strauberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAHS3409.1; -;
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Alignment Scores:
Pred. No.: 37.8 Length: 614
Score: 67.30 Matches: 12
Percent Similarity: 58.62% Conservative: 5
Best Local Similarity: 41.38% Mismatches: 5
Query Match: 45.47% Indels: 7
DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x Q7TWT6 (1-614)

QY 4 ATCTATCTGTCGACTCTGATACACATACAGCCGTCCTTCCAGGCGCGAGTCAG 63
Db 70 ValTyrProGlyAspGlyAspThrAsnTyrAsnGlyLysPheLysGlyLeuAlaThr--- 88

QY 64 GGTATTAGCAGCT 76
Db 89 ----LeuThrAla 91

RESULT 6

ID Q919C3 PRELIMINARY; PRT; 302 AA.
AC Q919C3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Sodium/potassium-transporting ATPase beta-233 chain (sodium/potassium-
dependent ATPase beta-233 subunit).
GN Name=atnb233;
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7936;
RN [1]_TaxID=7936;
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Gill;
RX PubMed=10896885;
RA Cutler C.P., Brezillon S., Bekir S., Sanders I.L., Hazon N., Cramb G.;
RT "Expression of a duplicate Na,K-ATPase beta(1)-isoform in the European
eel (Anguilla anguilla).";
RL Am. J. Physiol. 279:R222-R229(2000).
CC -!- FUNCTION: This is the non-catalytic component of the active
CC enzyme, which catalyzes the hydrolysis of ATP coupled with the
CC exchange of Na(+) and K(+) ions across the plasma membrane.
CC -!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
CC gamma.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed mainly in epithelial tissues.
CC -!- SIMILARITY: Belongs to the Na+/K+ and H+/K+ ATPases beta chain
CC family.
DR EMBL; AJ239317; CAB85586.1; -;
DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; NAS.

DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; NAS.
DR GO; GO:0006813; P:potassium ion transport; NAS.
DR GO; GO:0006814; P:sodium ion transport; NAS.
DR InterPro; IPR004042; Na/K-ATPase_beta.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR TIGRFAMS; TIGR01107; Na_K-ATPase bet; 1.
DR PROSITE; PS00390; ATPASE_NA_K_BETA_1; 1.
DR PROSITE; PS00391; ATPASE_NA_K_BETA_2; 1.
KW Glycoprotein; Signal-anchor; Sodium/potassium transport;
KW Transmembrane.
FT DOMAIN 1 33 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 34 54 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 55 302 EXTRACELLULAR (POTENTIAL).
FT DISULFID 125 148 By similarity.
FT DISULFID 158 174 By similarity.
FT DISULFID 213 274 By similarity.
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 302 AA; 34706 MW; 721E056F04274D0D CRC64;

Alignment Scores:
Pred. No.: 79.1 Length: 302
Score: 64.40 Matches: 14
Percent Similarity: 26.15% Conservative: 3
Best Local Similarity: 21.54% Mismatches: 2
Query Match: 42.37% Indels: 46
DB: 2 Gaps: 2

NOLAN463-2A.SEQ (1-84) x Q919C3 (1-302)

QY 61 GACTCGCCGCGC-----CTTGGG 44
Db 6 AspSerAspGlyGlyTyrLysThrPheLeuTrpAsnSerGluLysLysGluLeuLeuGly 25
QY 43 AGGACGGCGCTGATGTGTGATATCAG----- 20
Db 26 ArgThrGlyCysSerTrpPheLysLeuLeuPheTyrValIlePheTyrGlyCysLeu 45
QY 20 ----- 20
Db 46 AlaAlaValPheValGlyThrIleGlnAlaLeuLeuLeuThrLeuSerAsnTyrLysPro 65
QY 19 AGTCACCCAGGATAGA 5
Db 66 ThrHisGlnAspArg 70

RESULT 7

ID KV11_HUMAN
AC KV11_HUMAN STANDARD; PRT; 117 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";

```

RL Cell 32:181-189(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01322; AAA58930.1; -
DR EMBL; K01324; AAA58932.1; -
DR EMBL; V00558; CAA23824.1; -
DR PIR; A01881; KIHU11.
DR HSP; P01607; LBWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00447; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL.
FT CHAIN.
FT DOMAIN 23 >117
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 >117
FT DISULFID 45 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;

Alignment Scores:
Pred. No.: 86 Length: 117
Score: 63.60 Matches: 17
Percent Similarity: 45.24% Conservative: 2
Best Local Similarity: 40.48% Mismatches: 9
Query Match: 42.97% Indels: 14
DB: 1 Gaps: 2

NOLAN463-2A-SEQ (1-84) x KV11_HUMAN (1-117)
QY 1 ATCATCTATCTCGGT-----GACTCTGATACACATACAGCCGCTCC----- 42
Db 15 LeuCysPheProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSer 34
QY 43 -----TTCCAAGCGCGGAGTCAGGGTATTAGCAGCTGG 78
Db 35 AlaSerValGlyAspArgValThrIleThrCysArgAlaArgGlnGlyIleSerSerTrp 54
QY 79 TTAGCC 84
Db 55 LeuAla 56

RESULT 8
Q6PIH7
ID Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Lung;

```

```

RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -
DR HSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Alignment Scores:
Pred. No.: 96.2 Length: 236
Score: 63.60 Matches: 18
Percent Similarity: 48.72% Conservative: 1
Best Local Similarity: 46.15% Mismatches: 6
Query Match: 42.97% Indels: 14
DB: 2 Gaps: 2

NOLAN463-2A-SEQ (1-84) x Q6PIH7 (1-236)
QY 10 CCTCGT-----GACTCTGATACACATACAGCCGCTCCAGGC----- 51
Db 18 ProGlyAlaArgCysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerVal 37
QY 52 -----CGGCGGAGTCAGGGTATTAGCAGCTGGTAGCC 84
Db 38 GlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAla 56

RESULT 9
Q7Q1B6
ID Q7Q1B6 PRELIMINARY; PRT; 473 AA.
AC Q7Q1B6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP8180 (Fragment).
GN Name=agCG51167; ORFNames=ENSANGG00000012318;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAINS-PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC !- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008980; EAA14419.1; -.
DR InterPro; IPR005654; AFG1_ATPase.
DR Pfam; PF03969; AFG1_ATPase; 1.
FT NON_TER 1
SQ SEQUENCE 473 AA; 53210 MW; 6F8197395A1C7F79 CRC64;

Alignment Scores:
Pred. No.: 111 Length: 473
Score: 63.50 Matches: 13
Percent Similarity: 44.74% Conservative: 4
Best Local Similarity: 34.21% Mismatches: 6
Query Match: 42.91% Indels: 15
DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x Q7Q1B6 (1-473)
QY 1 ATCTATCTCTGGTGACTCTGATACCATACATACAGCCGCTCTTCCAAAGCGCGGCGAGT 60
Db ValValTyr-----AspSerIleGlyLysThrPheSerPro-----ProLysPro-----Ser 98
QY 61 CAGGGTATTAGCAGCTGGTTAGCC 84
Db ThrGlyIleGlyLysTrpPheSer 106

RESULT 10
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281 (1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSP; P01820; IG70.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region VH58 A1/A4.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN

FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Alignment Scores:
Pred. No.: 126 Length: 117
Score: 62.30 Matches: 12
Percent Similarity: 55.17% Conservative: 4
Best Local Similarity: 41.38% Mismatches: 6
Query Match: 42.09% Indels: 7
DB: 1 Gaps: 0

NOLAN463-2A.SEQ (1-84) x HV52_MOUSE (1-117)
QY 4 ATCTATCTCTGGTGACTCTGATACCATACATACAGCCGCTCTTCCAAAGCGCGGCGAGT 63
Db IleTyrProGlyAspGlySerThrLysTyrAsnGluLysPheLysGlyLeuAlaThr---- 88
QY 64 GGTATTAGCAGCT 76
Db LeuThrAla 91

RESULT 11
Q6TL49
ID Q6TL49 PRELIMINARY; PRT; 436 AA.
AC Q6TL49;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN Name=rbcl;
OS Glycexia fluitans.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Melicaceae; Glyceria.
OX NCBI_TaxID=254778;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolphin K.P., Joseph J.A., Fay M.F., Purvis A., Gowing D.,
RA Crawley M.J., Cowan R.S.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Rubisco catalyzes two reactions: the carboxylation of D-
CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
CC carbon dioxide fixation, as well as the oxidative fragmentation of
CC the pentose substrate in the photorespiration process. Both
CC reactions occur simultaneously and in competition at the same
CC active site (By similarity).
CC !- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
CC 2 3-phospho-D-glycerate.
CC !- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
CC phospho-D-glycerate + 2-phosphoglycolate.
CC !- SUBUNIT: 8 large chains + 8 small chains (By similarity).
CC !- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC !- SIMILARITY: Belongs to the Rubisco large chain family.
DR EMBL; AY395539; AAR38681.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR GO; GO:0009853; P:photorespiration; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR000685; Rubisco_large.
DR Pfam; PF00016; Rubisco_large; 1.
DR Pfam; PF02788; Rubisco_large; 1.
DR PROSITE; PS00157; RUBISCO_LARGE; 1.
KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
```

KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER 1
 FT NON_TER 436
 SQ SEQUENCE 436 AA; 48417 MW; 229C3E9FFCE4420B CRC64;

Alignment Scores:
 Pred. No.: 160 Length: 436
 Score: 62.20 Matches: 13
 Percent Similarity: 39.47% Conservative: 2
 Best Local Similarity: 34.21% Mismatches: 5
 Query Match: 42.03% Indels: 18
 DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x Q6TL49 (1-436)

QY 7 TATCTGCTGACTCTGATACACATACAGCCGCTCTTCCAGGCGCGCAGTCAGGCT 66
 |||||
 Db 61 TyrLyAGLyArGcys--TyrHisIleGluProVal-----ProGlyGluGluGly- 76
 |||||
 QY 67 ATTACAGCTGTTAGCC 84
 |||||
 Db 77 -----GlnTrpIleAla 80
 |||||

RESULT 12

Q72WG5
 ID Q72WG5 PRELIMINARY; PRT; 138 AA.

AC Q72WG5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Sigma factor serine-protein kinase.
 GN OrderedLocusNames=DVUA0124;
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
 CG Plasmid pdv
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobivirionales;
 OC Desulfobivirionaceae; Desulfobivrio.
 OX NCBI_TaxID=882;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15077118; DOI=10.1038/nbr959;
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
 RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Davidgen T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 Desulfovibrio vulgaris Hildenborough."
 RL Nat. Biotechnol. 22:554-559(2004).
 DR EMBL; AB017286; AAS94340.1; -;
 DR TIGR; DVUA0124; -;
 KW Complete proteome.

SQ SEQUENCE 138 AA; 15178 MW; 0878CD5858774397 CRC64;

Alignment Scores:
 Pred. No.: 141 Length: 138
 Score: 62.00 Matches: 12
 Percent Similarity: 41.38% Conservative: 0
 Best Local Similarity: 41.38% Mismatches: 7
 Query Match: 40.79% Indels: 10
 DB: 2 Gaps: 0

NOLAN463-2A.SEQ (1-84) x Q72WG5 (1-138)

QY 67 TACCTGACTCCCGCGCTTGGAGGACGGGCTGTATGTGTATGATCAGATCACCAGGAT 8
 |||||
 Db 51 TyrProApsSerProGlyLysAlaGluValGlyCys-----ArgValValLeuPh 67
 |||||
 QY 7 AGATGAT 1
 |||||
 Db 67 eAspAep 69
 |||||

RESULT 13

Q8MT62
 ID Q8MT62 PRELIMINARY; PRT; 984 AA.

AC Q8MT62;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RE04357P.
 GN ORFNames=CG10353;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY118358; AAM48387.1; -;
 DR FLYBase; FBgn0030349; CG10353.
 DR InterPro; IPR007632; DUF590.
 DR Pfam; PF04547; DUF590; 1
 SQ SEQUENCE 984 AA; 112356 MW; 233EFCAAD0405E8 CRC64;

Alignment Scores:

Pred. No.: 205 Length: 984
 Score: 61.80 Matches: 13
 Percent Similarity: 55.88% Conservative: 6
 Best Local Similarity: 38.24% Mismatches: 3
 Query Match: 40.66% Indels: 12
 DB: 2 Gaps: 1

NOLAN463-2A.SEQ (1-84) x Q8MT62 (1-984)

QY 77 CAGCTGCTATACCTGACTCGCCGCGCTTGGAGGAC-----GGGCTG 33
 ::::|||||
 Db 685 GluMetLeuIleProTyrLeuMetArgThrPhelysGluLeuSerTyrArgHisGly--- 703
 :|||
 QY 32 TATGTGGTATCAGAGTCACAGGATAGA 5
 |||||:|||||
 Db 704 ---TriPtyrlySerHisGlnAepGln 711
 |||||:|||||

RESULT 14

Q9VYS8
 ID Q9VYS8 PRELIMINARY; PRT; 1043 AA.

AC Q9VYS8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG10353-PA.
 GN ORFNames=CG10353;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champ E., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003487; AAF48110.2; --
DR IntAct; Q9VYS8; --
DR FlyBase; FBgn0030349; CG10353.
DR InterPro; IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
SQ SEQUENCE 1043 AA; 118845 MW; 0EA6BDC5C219FF35 CRC64;
Alignment Scores:
Pred. No.: 207 Length: 1043
Score: 61.80 Matches: 13
Percent Similarity: 55.88% Conservative: 6
Best Local Similarity: 38.24% Mismatches: 3
Query Match: 40.66% Indels: 12
DB: 2 Gaps: 1
NOLAN463-2A.SEQ (1-84) x Q9VYS8 (1-1043)
QY 77 CAGCTGCTAATACCTGACTGCCTCCGCGCTTGGAGGAC-----GGGCTG 33
Db 744 GluMetLeuIleProTyLeuMetArgThrPhelYsGluLeuSerTyArgHisGly--- 762
QY 32 TATGTGTATCAGAGTCACAGGATAGA 5
Db 763 ----TriTyLysSerHisGlnAspGln 770
RESULT 15
Q76NS2 PRELIMINARY; PRT; 1059 AA.
ID Q76NS2
AC Q76NS2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG10353-PB.
GN ORFNames=CG10353;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

Search completed: August 4, 2005, 19:01:24
Job time : 87.75 secs

```
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleeb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003487; AAN09305.2; -.
DR InterPro; IPR007632; DUF590.
DR Pfam; PF04547; DUF590; 1.
SQ SEQUENCE 1059 AA; 120767 MW; 676365606C1CA98A CRC64;

Alignment Scores:
Pred. No.:      207      Length:      1059
Score:          61.80      Matches:      13
Percent Similarity: 55.88%      Conservative: 6
Best Local Similarity: 38.24%      Mismatches: 3
Query Match:      40.66%      Indels:      12
DB:              2          Gaps:      1

NOLAN463-2A.SEQ (1-84) x Q76NS2 (1-1059)

QY 77 CAGCTGCTATACCTGACTGCCCGCTTGAGAGAC-----GGGCTG 33
Db 760 GluMetLeuIleProTyrLeuMetArgThrPheLysGluLeuSerTyrArgHisGly--- 778
QY 32 TATGTGGTATCAGAGTCACCGAGATAGA 5
Db 779 ----TrpTyrLysSerHisGlnAspGln 786
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:21:34 ; Search time 90 Seconds
(without alignments)
721.953 Million cell updates/sec

Title: NOLAN463-2B.SEQ
Perfect score: 148
Sequence: 1 CGGGGAGTCAGGTATTAG.....ACAGCCCGCTCTTCCAGGC 84

Scoring table:
BLOSUM62 Xgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/NOLAN08728463-2/runat_04082005_123943_22574/app.query.fasta_1.5
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 115 | 77.7 | 123 | 5 | ABG76561 HCV E1 an |
| 2 | 113.3 | 76.6 | 411 | 8 | ADr46829 Human pB1 |
| 3 | 106.2 | 71.8 | 122 | 4 | Aau02582 Anti-adip |
| 4 | 104.4 | 70.5 | 474 | 4 | Aau14177 Human nov |
| 5 | 103.4 | 69.9 | 98 | 2 | Aaw54008 Human Ant |
| 6 | 103.4 | 69.9 | 98 | 5 | ABG78233 Human Fv |
| 7 | 103.4 | 69.9 | 98 | 5 | ABG78231 Human Fv |
| 8 | 103.4 | 69.9 | 98 | 5 | ABG78232 Human Fv |
| 9 | 103.4 | 69.9 | 98 | 5 | ABG91924 Human ant |
| 10 | 103.4 | 69.9 | 98 | 5 | ABG91922 Human ant |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 11 | 103.4 | 69.9 | 98 | 5 | ABG91923 | Abg91923 Human ant |
| 12 | 103.4 | 69.9 | 98 | 6 | ABU56809 | Abu56809 Human Imm |
| 13 | 103.4 | 69.9 | 98 | 6 | ABP56508 | Abp56508 Human ant |
| 14 | 103.4 | 69.9 | 98 | 6 | ABJ18687 | Abj18687 Antibody |
| 15 | 103.4 | 69.9 | 98 | 6 | ABO27112 | AbO27112 Human ger |
| 16 | 103.4 | 69.9 | 98 | 7 | ADG69247 | Adg69247 Human hea |
| 17 | 103.4 | 69.9 | 98 | 7 | ADF10156 | Adf10156 Antibody |
| 18 | 103.4 | 69.9 | 98 | 7 | ADF09948 | Adf09948 Antibody |
| 19 | 103.4 | 69.9 | 98 | 7 | ADF10053 | Adf10053 VEGF anti |
| 20 | 103.4 | 69.9 | 98 | 7 | ADK18943 | Adk18943 Anti-huma |
| 21 | 103.4 | 69.9 | 98 | 7 | ADK18888 | Adk18888 Anti-huma |
| 22 | 103.4 | 69.9 | 98 | 7 | ADK18877 | Adk18877 Anti-huma |
| 23 | 103.4 | 69.9 | 98 | 7 | ADK18878 | Adk18878 Anti-huma |
| 24 | 103.4 | 69.9 | 98 | 7 | ADK18912 | Adk18912 Anti-huma |
| 25 | 103.4 | 69.9 | 98 | 7 | ADK18582 | Adk18582 Anti-huma |
| 26 | 103.4 | 69.9 | 98 | 7 | ADK18896 | Adk18896 Anti-huma |
| 27 | 103.4 | 69.9 | 98 | 7 | ADK18894 | Adk18894 Anti-huma |
| 28 | 103.4 | 69.9 | 98 | 7 | ADJ80328 | Adj80328 VH gene 1 |
| 29 | 103.4 | 69.9 | 98 | 8 | ADR46847 | Adr46847 Human VHS |
| 30 | 103.4 | 69.9 | 109 | 8 | ADI05782 | Adi05782 Human mon |
| 31 | 103.4 | 69.9 | 109 | 8 | ADP22377 | Adp22377 Human ant |
| 32 | 103.4 | 69.9 | 109 | 8 | ADP22385 | Adp22385 Human ant |
| 33 | 103.4 | 69.9 | 109 | 8 | ADS12513 | Ads12513 Human VHS |
| 34 | 103.4 | 69.9 | 109 | 8 | ADS12515 | Ads12515 Human VHS |
| 35 | 103.4 | 69.9 | 109 | 8 | ADS12514 | Ads12514 Human VHS |
| 36 | 103.4 | 69.9 | 110 | 8 | ADP47302 | Adp47302 Human pho |
| 37 | 103.4 | 69.9 | 113 | 6 | ABU08149 | Abu08149 Human Erb |
| 38 | 103.4 | 69.9 | 113 | 7 | ADD69211 | Add69211 Human ant |
| 39 | 103.4 | 69.9 | 116 | 8 | ADP22194 | Adp22194 Human ant |
| 40 | 103.4 | 69.9 | 117 | 2 | AAR66339 | Aar66339 Human Imm |
| 41 | 103.4 | 69.9 | 117 | 4 | AAG62966 | Aag62966 Amino aci |
| 42 | 103.4 | 69.9 | 117 | 5 | AAO15186 | Aao15186 Digi anti |
| 43 | 103.4 | 69.9 | 117 | 6 | ABP97450 | Abp97450 Human ant |
| 44 | 103.4 | 69.9 | 117 | 8 | ADL70771 | Adl70771 Anti-TNFA |
| 45 | 103.4 | 69.9 | 117 | 8 | ADP47229 | Adp47229 Human pho |

ALIGNMENTS

RESULT 1
ABG76561
ID ABG76561 standard; protein; 123 AA.

XX AC ABG76561;
XX DT 05-NOV-2002 (first entry)
XX DE HCV E1 antigen monoclonal antibody #49.
XX KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
XX KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
XX OS Homo sapiens.
XX FN WO200260954-A1.
XX PD 08-AUG-2002.
XX PF 14-JAN-2002; 2002WO-SE0000044.
XX PR 12-JAN-2001; 2001US-0260889P.
XX PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX PI Drakenberg K, Persson MAA;
XX DR WPI; 2002-608502/65.
XX PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
XX PS (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX Disclosure; Page 54; 64pp; English.

CC The invention relates to a human monoclonal antibody or its antigen
CC binding fragments, which exhibit immunological binding affinity for a
CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
CC homologous to the binding portion of a human antibody Fab molecule from a
CC combinatorial antibody library. The vaccine composition comprising the
CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
CC its hypervariable region is useful in treating or preventing HCV
CC infection in a subject. Sequences ABG76513-ABG76568 represent human
CC monoclonal antibodies against HCV E1 antigen
XX
SQ Sequence 123 AA;

Alignment Scores:

Pred. No.: 7,058-05 Length: 123
Score: 115.00 Matches: 23
Percent Similarity: 55.32% Conservative: 3
Best Local Similarity: 48.94% Mismatches: 1
Query Match: 77.70% Indels: 20
DB: 5 Gaps: 1

NOLAN463-2B-SEQ (1-84) x ABG76561 (1-123)

QY 1 CCGGCGAGT----- 9
DB 25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44
QY 10 CAGGTATTAGCAGCTGGTTAGCCATCATCTATCTCTGGTGACTCTGTATACCATACAGC 69
DB 45 GlnGlyLeu---GluTrpMetAlaIleIleTyrProGlyAspSerAspThrThrTyrSer 63
QY 70 CGGCTCTCCAGGC 84
DB 64 ProSerPheGluGly 68

RESULT 2

ADR46829

ID ADR46829 standard; protein; 411 AA.

XX ADR46829;

XX 18-NOV-2004 (first entry)

XX Human pB11-betahCG molecular conjugate protein SEQ ID NO:12.

XX molecular conjugate; monoclonal antibody; human antigen presenting cell;
XX antigen presenting cell; APC; human; beta human chorionic gonadotropin;
XX betahCG; beta chorionic gonadotropin; antibody;
XX T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
XX immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
XX CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
XX melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
XX antibody B11; pB11-betahCG molecular conjugate; fusion protein.

OS Homo sapiens.

OS Synthetic.

XX WO2004074432-A2.

XX 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US002725.

XX 31-JAN-2003; 2003US-0443979P.

XX (MEDA-) MEDAREX INC.

XX Keler T, Endres M, He L, Ramakrishna V;

XX WPI; 2004-635555/61.

XX N-PSDB; ADR46828.

XX New molecular conjugate having a monoclonal antibody that binds to human
XX APCs linked to a beta human chorionic gonadotropin, useful for inducing a

PT cytotoxic T cell response in cancers and infectious diseases.

XX Claim 16; SEQ ID NO 12; 82pp; English.

XX The present invention describes a molecular conjugate comprising a
CC monoclonal antibody that binds to human antigen presenting cells (APCs)
CC linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC comprises a heavy and/or light chain variable region derived from a human
CC VHS-51 or Vh-L15 germline sequence with the 98 or 95 amino acid sequences
CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also
CC described: (1) a molecular conjugate comprising a human antibody heavy
CC chain and a human antibody light chain, where either or both chains are
CC linked to betahCG; (2) a molecular conjugate comprising a human single
CC chain antibody that binds to human APCs linked to betahCG, where the
CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12
CC (ADR46829); (3) a composition comprising any of the molecular conjugates
CC as described above, and a carrier, optionally in combination with an
CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,
CC against betahCG, comprising contacting any of the molecular conjugates
CC described above with APCs such that the antigen is processed and
CC presented to T cells in a manner which induces or enhances a T cell-
CC mediated response against the antigen; (5) immunising a subject
CC comprising administering any of the molecular conjugates described above,
CC optionally in combination with an adjuvant, a cytokine which stimulates
CC proliferation of dendritic cells and/or an immunostimulatory agent; and
CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,
CC comprising forming a conjugate of the antigen and a monoclonal antibody
CC which binds to APCs, and contacting the conjugate either in vivo or ex
CC vivo with APCs such that the antigen is internalised, processed and
CC presented to T cells in a manner which induces or enhances a cytotoxic T
CC cell response against the antigen. The molecular conjugate has
CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,
CC virucide and antimalarial activities, and can be used as a CD8 agonist,
CC and in vaccines. The methods and compositions of the present invention
CC are useful for inducing a cytotoxic T cell response, and in particular
CC for treating autoimmune disorders, cancers and infectious diseases by
CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,
CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria and
CC herpes. The present sequence represents a human pB11-betahCG molecular
CC conjugate, which is used in the exemplification of the present invention.

XX Sequence 411 AA;

Alignment Scores:

Pred. No.: 0.000163 Length: 411
Score: 113.30 Matches: 26
Percent Similarity: 15.76% Conservative: 0
Best Local Similarity: 15.76% Mismatches: 2
Query Match: 76.55% Indels: 137
DB: 8 Gaps: 1

NOLAN463-2B-SEQ (1-84) x ADR46829 (1-411)

QY 1 CCGGCGAGTCAAGGTATTAGCAGCTGGTTAGCC----- 33

DB 43 ArgAlaSerGlnGlyIleSerArgTrpLeuAlaTrpTyrGlnGlnLysProGlnLysAla 62

QY 33 ----- 33

DB 63 ProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 82

QY 33 ----- 33

DB 83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnProGlnAspPhe 102

QY 33 ----- 33

DB 103 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProArgThrPheGlyGlnGlyThrLys 122

QY 33 ----- 33

DB 123 ValGluIleLysGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlu 142

QY 33 ----- 33
Db 143 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuArgIleSer 162
QY 33 ----- 33
Db 163 CysLysGlySerGlyAspSerPheThrThrTyrTyrTrpIleGlyTyrPValArgGlnMetPro 182
QY 34 -----ATCATCTATPCTGGTGACTCTGATACACATACAGC 69
Db 183 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyrSer 202
QY 70 CCGTCTCTCCAGGC 84
Db 203 ProSerPheGlnGly 207
RESULT 3
AAU02582
ID AAU02582 standard; protein; 122 AA.
XX
AC AAU02582;
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody heavy chain, FAT 69.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
XX
DR N-PSDB; AAS03482.
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Claim 1; Page 144; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 122 AA;

Alignment Scores:

Pred. No.: 0.000801 Length: 122
Score: 106.20 Matches: 20
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 60.61% Mismatches: 3
Query Match: 71.76% Indels: 8
DB: Gaps: 0
NOLAN463-2B-SEQ (1-84) x AAU02582 (1-122)
QY 2 GGGCCAGTCAGGCTATTAGCAGCTGGTTAGCCATCATCTATCTGGTCACTCTGATACCA 61
Db 42 GlyArg-----GlyLeu---GluTrpMetGlyIleIleTyrProGlyAspSerAspThrA 59
QY 62 CATACAGCCCGTCTTCCAGGC 84
Db 59 rgTyrSerProSerPheGlnGly 66
RESULT 4
AAU14177
ID AAU14177 standard; protein; 474 AA.
XX
AC AAU14177;
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #48.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002623.
XX
PR 25-JAN-2000; 2000US-00491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
DR N-PSDB; AAS22482.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Example 4; Page 554-555; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human proteins or
CC their active domains. The polypeptides, polynucleotides and antibodies
CC raised against the polypeptides are used in a method of treatment of a
CC mammal and prevention of disorders caused by the aberrant protein
CC expression or activity. The polypeptides can be used as molecular weight
CC markers, food supplements, and in antibody production. The polypeptides
CC are used to identify compounds which bind to the polypeptides.
CC Polynucleotides of the invention are used as probes and primers, for
CC sequencing, for chromosome or gene mapping, in the production of
CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
CC therapy. Polypeptides of the invention can be used to target drugs to a
CC tumour, in assays to determine biological activity, to raise
CC antibodies/elicit an immune response, to determine quantitative protein
CC levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention
 XX
 SQ Sequence 474 AA;

Alignment Scores:
 Pred. No.: 0.00199 Length: 474
 Score: 104.40 Matches: 23
 Percent Similarity: 47.17% Conservative: 2
 Best Local Similarity: 43.40% Mismatches: 2
 Query Match: 70.54% Indels: 26
 DB: 4 Gaps: 2

NOLAN463-2B-SEQ (1-84) x AAU14177 (1-474)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21
 DB 34 GlyGluSerValLysIleSerCysLysGlySerGlyTyr-SerPheSerAspTyrTrpVa 53
 QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
 DB 53 lAlaTrpValArgGlnSerProAspLysGlyLeuAlaTrpMetGlyIleIleTyrProGl 73
 QY 48 TGACTCTGATACCATACAGCCGCTCTTCCAAAGGC 84
 DB 73 yAspSerAspThrArGlyTyrSerProSerPheGlnGly 85

RESULT 5

AAW54008
 ID AAW54008 standard; protein; 98 AA.

XX
 AC AAW54008;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-JUL-1998 (first entry)
 XX
 DE Human Anti-CD4 antibody VH5 consensus sequence.

XX Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 KW Old World monkey; constant domain; eczema; immuno-modulated disease;
 KW rheumatoid arthritis.

XX Homo sapiens.
 XX US5750105-A.
 XX
 PD 12-MAY-1998.

XX
 PF 07-JUN-1995; 95US-00476349.
 XX
 PR 25-JUL-1991; 91US-00735064.
 PR 23-MAR-1992; 92US-00856281.
 PR 10-JUL-1992; 92US-00912292.
 PR 25-JAN-1995; 95US-00379072.

XX (IDEC-) IDEC PHARM CORP.

XX Raab RW, Newman RA, Hanna N;
 XX WPI; 1998-296690/26.
 DR

XX Improved method for antibody treatment - uses an antibody comprising an
 PT Old World monkey variable region and a human constant domain.
 XX
 PS Example 1; Fig 9e; 84pp; English.

CC This sequence is the consensus VH5 domain of an anti-CD4 antibody (Ab).
 CC This sequence can be used in the method of the invention for treating a
 CC subject, where the treatment comprises administration of an Ab. The
 CC method comprises the administration of an antibody which has an Old World
 CC monkey (e.g. baboon or macaque) variable region which binds to an antigen
 CC (Ag) for Ag binding portion, and a human constant domain. The method is
 CC useful for the treatment of eczema and immuno-modulated diseases and
 CC especially rheumatoid arthritis. The recombinant antibodies used are
 CC sufficiently different from native monkey antibodies to allow human
 CC antigens to raise these antibodies, but similar enough to human antibody
 CC so there is no immune response to the antibodies in humans. Compared to
 CC human anti-antibodies on repeated administration. They also have longer
 CC half-lives and do not have a lack of effector function with human cells.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

SQ Sequence 98 AA;

Alignment Scores:
 Pred. No.: 0.00163 Length: 98
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 2 Gaps: 2

NOLAN463-2B-SEQ (1-84) x AAW54008 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21
 DB 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
 QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
 DB 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
 QY 48 TGACTCTGATACCATACAGCCGCTCTTCCAAAGGC 84
 DB 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 6

ABG78233
 ID ABG78233 standard; protein; 98 AA.

XX AC ABG78233;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #108.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding

PT characteristics so as to selectively bind target cell in favor of other
 XX cells.
 XX
 XX Claim 13; Page 205; 232pp; English.
 XX
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (dsFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 98 AA;

Alignment Scores:
 Pred. No.: 0.00163 Length: 98
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 5 Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABG78233 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21
 Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
 QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
 Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyr-ProG1 54
 QY 48 TGACTCTGTATACCATACAGCCGCTCTTCCAGGC 84
 Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 7

ABG78231
 ID ABG78231 standard; protein; 98 AA.

XX ABG78231;
 XX
 XX 15-NOV-2002 (first entry)
 XX
 XX Human Fv molecule hypervariable region related peptide #106.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.

XX WO200259264-A2.
 XX
 XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US049440.
 XX
 XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;

XX WPI; 2002-619166/66.
 XX
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 XX cells.
 XX
 XX Claim 13; Page 204; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (dsFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 98 AA;

Alignment Scores:
 Pred. No.: 0.00163 Length: 98
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 5 Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABG78231 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21
 Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
 QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
 Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyr-ProG1 54
 QY 48 TGACTCTGTATACCATACAGCCGCTCTTCCAGGC 84
 Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 8

ABG78232
 ID ABG78232 standard; protein; 98 AA.

XX ABG78232;
 XX
 XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #107.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.

XX WO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US049440.

XX 29-DEC-2000; 2000US-00751181.

```
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX Plaksin D, Peretz T;
XX
XX WPI; 2002-619166/66.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX or fragment, or construct of fragment with enhanced binding
XX characteristics so as to selectively bind target cell in favor of other
XX cells.
XX
XX Claim 13; Page 204-205; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
XX molecule, a construct or fragments or a construct of a fragment with
XX enhanced binding characteristics which selectively and/or specifically
XX binds to a target cell in favour of other cells, where binding is
XX primarily determined by a first hypervariable region and Fv is a single
XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX association with or attached, coupled, combined, linked or fused to a
XX pharmaceutical agent, is useful in the manufacture of a medicament, where
XX the medicament has activity against a diseased cell, preferably a cancer
XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX composition for use in inhibiting the growth of a diseased or cancer
XX cell. This sequence represents a human Fv molecule hypervariable region
XX related peptide of the invention
XX
XX Sequence 98 AA;
XX
XX Alignment Scores:
XX Pred. No.: 0.00163 Length: 98
XX Score: 103.40 Matches: 23
XX Percent Similarity: 45.28% Conservative: 1
XX Best Local Similarity: 43.40% Mismatches: 3
XX Query Match: 69.86% Indels: 26
XX DB: 5 Gaps: 2
XX
XX NOLAN463-2B.SEQ (1-84) x ABG78232 (1-98)
XX
XX QY 3 GCGAGTCA-----GGGTATTAGC----- 21
XX Db 15 GlyGluserLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
XX
XX QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
XX Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
XX
XX QY 48 TGACTCTGATACACATACAGCCGCTCTCCAAAGC 84
XX Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
XX
XX RESULT 9
XX ABG91924
XX ID ABG91924 standard; protein; 98 AA.
XX
XX AC ABG91924;
XX
XX DT 04-DEC-2002 (first entry)
XX
XX DE Human antibody fragment #108.
XX
XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
XX retencoid; leukaemia; inflammatory disease; cardiovascular disease;
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX sulphated tyrosine-dependent protein-protein interaction.
XX
XX OS Homo sapiens.
XX
XX
```

```
FN WO200253700-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 31-DEC-2001; 2001WO-US049442.
XX
XX PR 29-DEC-2000; 2000US-00751181.
XX
XX PR 29-DEC-2000; 2000US-0258948P.
XX
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
XX WPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
XX physiological phenomena such as cell rolling, metastasis and
XX inflammation, for treating autoimmune, inflammatory or cardiovascular
XX diseases, and cancer.
XX
XX Disclosure; Page 281; Opp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
XX important in physiological phenomena such as cell rolling, metastasis and
XX inflammation, where the epitope is capable of being bound by an antibody,
XX its antigen-binding fragment or its complex comprising at least one
XX antibody or its binding fragment having a first hypervariable region. The
XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
XX disease, thrombosis, restenosis, metastasis, growth and/or replication of
XX tumour or leukaemia cells, increase in number of tumour or leukaemia
XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
XX platelet and/or cell-platelet adhesion or aggregation, for increasing
XX mortality of tumour or leukaemia cells, for increasing the susceptibility
XX of diseased cells to damage by anti-disease, anti-cancer or anti-
XX leukaemia agents, or for decreasing the number of tumour or leukaemia
XX cells in a patient, or in the manufacture of a medicament for the above
XX mentioned purposes. The epitopes are useful for diagnosing and treating
XX diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
XX diseases, cardiovascular diseases such as myocardial infarction,
XX retinopathic diseases and other diseases mediated by abnormal platelet
XX function and diseases caused by sulphated tyrosine-dependent protein-
XX protein interactions. This sequence represents a human antibody fragment
XX of the invention
XX
XX Sequence 98 AA;
XX
XX Alignment Scores:
XX Pred. No.: 0.00163 Length: 98
XX Score: 103.40 Matches: 23
XX Percent Similarity: 45.28% Conservative: 1
XX Best Local Similarity: 43.40% Mismatches: 3
XX Query Match: 69.86% Indels: 26
XX DB: 5 Gaps: 2
XX
XX NOLAN463-2B.SEQ (1-84) x ABG91924 (1-98)
XX
XX QY 3 GCGAGTCA-----GGGTATTAGC----- 21
XX Db 15 GlyGluserLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
XX
XX QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
XX Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
XX
XX QY 48 TGACTCTGATACACATACAGCCGCTCTCCAAAGC 84
XX Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
XX
XX RESULT 10
XX ABG91922
XX ID ABG91922 standard; protein; 98 AA.
XX
XX
```


SQ Sequence 98 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00163 | Length: | 98 |
| Score: | 103.40 | Matches: | 23 |
| Percent Similarity: | 45.28% | Conservative: | 1 |
| Best Local Similarity: | 43.40% | Mismatches: | 3 |
| Query Match: | 69.86% | Indels: | 26 |
| DB: | 5 | Gaps: | 2 |

NOLAN463-2B.SEQ (1-84) x ABG91923 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21

Db 15 GlyGluSerLeuIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47

Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAAGGC 84

Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 12

ABU56809

ID ABU56809 standard; protein; 98 AA.

AC ABU56809;

DT 03-APR-2003 (first entry)

DE Human Immunoglobulin heavy variable chain polypeptide #5.

KW Human; tumour; cancer; systemic lupus erythematosus;

KW immunoglobulin constant region; immunoglobulin variable region;

KW autoimmune response; rheumatoid arthritis; eczema; lymphoma;

KW immunomodulatory disease; leukaemia; Hashimoto's thyroiditis;

KW autoimmune carditis; Addison's disease; type I-diabetes mellitus;

KW multiple sclerosis; male infertility; autoimmune hemolytic anaemia;

KW inflammatory bowel disease; Sjogren's syndrome; psoriasis.

OS Homo sapiens.

XX

XX US2002150580-A1.

PN

XX 17-OCT-2002.

PD

XX 08-MAY-2001; 2001US-00850165.

PF

XX 25-JUL-1991; 91US-00735064.

PR

XX 23-MAR-1992; 92US-00856281.

PR

XX 10-JUL-1992; 92US-00912292.

PR

XX 25-JAN-1995; 95US-00379072.

PR

XX 07-JUN-1995; 95US-00476237.

PR

XX 21-MAY-1998; 98US-00082472.

XX

PA (IDEC-) IDEC PHARM CORP.

XX

XX Newman RA, Hanna N, Raab RW;

PI

XX WPI; 2003-182483/18.

DR

XX New recombinant chimeric antibodies comprising human, chimpanzee and Old

PT World monkey portions, useful for treating e.g. cancer, eczema, leukemia,

PT lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male

PT infertility.

XX

XX Disclosure; Fig 9E; 101pp; English.

PS

XX The invention describes a recombinant antibody comprising a human,

CC chimpanzee or a first Old World monkey immunoglobulin constant region,

CC and an antigen-binding portion of a second Old World monkey

CC

immunoglobulin variable region. The first and second Old World monkey can be the same or different. The recombinant antibody is useful for treating a human having the antigen described above, e.g. for treating cancer in an autoimmune response (where the antigen is involved in an autoimmune response in the human). In particular, the recombinant antibody is useful for treating rheumatoid arthritis, eczema, or an immunomodulatory disease. The recombinant antibody is also useful for treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis, Addison's disease, type I-diabetes mellitus, multiple sclerosis, male infertility, autoimmune hemolytic anaemia, inflammatory bowel disease, Sjogren's syndrome, psoriasis, or systemic lupus erythematosus. This is the amino acid sequence of a human immunoglobulin heavy variable chain polypeptide for creation of the recombinant antibody

SQ Sequence 98 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00163 | Length: | 98 |
| Score: | 103.40 | Matches: | 23 |
| Percent Similarity: | 45.28% | Conservative: | 1 |
| Best Local Similarity: | 43.40% | Mismatches: | 3 |
| Query Match: | 69.86% | Indels: | 26 |
| DB: | 6 | Gaps: | 2 |

NOLAN463-2B.SEQ (1-84) x ABU56809 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21

Db 15 GlyGluSerLeu**IleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34

QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47

Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54

QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAAGGC 84

Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 13

ABP56508

ID ABP56508 standard; protein; 98 AA.

XX

XX ABP56508;

XX

XX 20-MAR-2003 (first entry)

DT

XX Human anti-Fc-epsilon-R1 alpha autoantibody heavy chain VHVCW.

DE

XX Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;

KW allergic disease; urticaria; late phase allergic reaction; malignancy;

KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;

KW conditional autoimmunity; IgE mediated disease.

OS Homo sapiens.

OS Synthetic.

XX

XX WO200282085-A2.

PN

XX 17-OCT-2002.

PD

XX 03-APR-2002; 2002WO-EP003660.

PF

XX 04-APR-2001; 2001US-0281024P.

PR

XX (ZLBB-) ZLB BIOPLASMA AG.

PA

XX Miescher S;

PI

XX WPI; 2003-103348/09.

DR

XX Identifying and obtaining inhibitor of a pathological process for

PT treating e.g. autoimmunity comprises determining if a compound is capable

PT

PT of modulating the binding of the Fc-epsilon-R1 receptor and an
XX autoantibody against its alpha-chain.

PS Claim 20; Page 22; 29pp; English.

XX The present invention describes a method for identifying and obtaining an
CC inhibitor of a pathological process. The method comprises determining if
CC a compound is capable of modulating the binding of the Fc-epsilon-R1
CC receptor alpha-chain and an autoantibody against its alpha-chain. Also
CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor
CC alpha-chain for identifying and obtaining an inhibitor of a pathological
CC process; (2) use of the identified inhibitor for inhibiting activity of
CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3)
CC a compound identified by the method, which binds but does not activate
CC the receptor; and (4) a polypeptide capable of specific binding to the Fc
CC -epsilon-R1 receptor alpha-chain. The method is useful for obtaining an
CC inhibitor of a pathological process e.g. imbalance between cell-bound and
CC free IgE e.g. allergic disease (urticaria, late phase allergic reactions,
CC intrinsic asthma, drug intolerance and food intolerance), IgE mediated
CC disease or malignancy. The compound is useful for treating a pathological
CC process, particularly conditional autoimmunity. The present sequence
CC represents a human recombinant anti-Fc-epsilon-R1 alpha autoantibody
XX heavy chain protein sequence from the present invention
SQ Sequence 98 AA;

Alignment Scores:
Pred. No.: 0.00163 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 6 Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABP56508 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
DB 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
DB 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAAGGC 84
DB 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 14
ABJ18687
ID ABJ18687 standard; protein; 98 AA.

XX AC ABJ18687;

XX DT 06-MAR-2003 (first entry)

XX DE Antibody library related human protein sequence SEQ ID No 16.

XX KW Library; recombinant antibody; clustering variable region; in silico;
XX immunogenecity; antibody therapeutic; human.

XX OS Homo sapiens.

XX PN WO200284277-A1.

XX PD 24-OCT-2002.

XX PF 17-APR-2002; 2002WO-US012202.

XX PR 17-APR-2001; 2001US-0284407P.

XX PA (ABMA-) ABMAXIS INC.

PI Luo P;

XX DR WPI; 2003-093043/08.

XX PT Constructing a library of recombinant antibodies useful as source of
XX antibody candidates for screening antigens comprises clustering variable
XX regions of antibodies having known 3-dimensional structures into
XX structural ensembles.

XX PS Disclosure; Page 109-110; 119pp; English.

XX CC The invention relates to a novel method for the construction of a library
XX of recombinant antibodies. The novel method comprises clustering variable
XX regions of a collection of antibodies having known 3D structures into at
XX least two families of structural ensembles, each comprising at least two
XX different antibody sequences but with substantially identical main chain
XX conformations. The method is useful for constructing a library of
XX artificial antibodies in silico which provides a structurally diverse and
XX yet functionally more relevant source of antibody candidates which can
XX then be screened for binding a wide variety of target molecules,
XX including small molecules, and biomacromolecules such as proteins,
XX peptides and nucleic acids. The libraries constructed are useful as a
XX source of antibody candidates for further screening for novel antibodies
XX with high affinity against a wide range of antigens and having no or
XX minimum immunogenecity to human subjects treated with antibody
XX therapeutics. This sequence represents a human peptide region of an
XX antibody relating to the novel antibody library construction method of
XX the invention

SQ Sequence 98 AA;

Alignment Scores:
Pred. No.: 0.00163 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 6 Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABJ18687 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
DB 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
DB 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAAGGC 84
DB 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 15

ABO27112

ID ABO27112 standard; protein; 98 AA.

XX AC ABO27112;

XX DT 10-SEP-2003 (first entry)

XX DE Human germline heavy chain variable region gene segment #45.

XX KW Human; heavy chain variable region; VH; humanised antibody;
XX chimeric antibody; complementarity determining region; CDR;

XX OS Homo sapiens.

XX PN US2003039649-A1.

XX PD 27-FEB-2003.

XX XX

PF 12-JUL-2002; 2002US-00194975.
XX
PR 12-JUL-2001; 2001US-0305111P.
XX
PA (FOOT/) FOOTE J.
XX
PI Foote J;
XX
XX WPI; 2003-492151/46.
XX
XX Making humanized antibody for converting antibody, by making chimeric
PT antibodies containing complementarity determining region from non-human
PT antibody and appropriate framework sequences of human antibodies.
XX
XX Example 1; Fig 1; 31pp; English.
XX
CC The invention describes a method of making a humanised antibody,
CC comprising making chimeric antibodies containing a complementarity
CC determining region (CDR) from a non-human antibody and appropriate
CC framework sequences (I) of human antibodies. (I) is selected by using
CC canonical CDR structure types of non-human antibody in comparison to
CC germline canonical CDR structure types of human antibodies as the basis
CC for selection, for humanisation. The method is useful for making a
CC humanised antibody or a converted antibody. The method is applicable for
CC converting a subject antibody sequence of any subject species to a less
CC immunogenic form suitable for use in an object species. The method is
CC reliable for identifying suitable human framework sequences to support
CC non-human CDR regions and to provide humanised antibodies that retain
CC high antigen binding with low immunogenicity in humans, without the need
CC for direct comparison of framework sequences, without the need for
CC determining critically important amino acid residues in the framework,
CC and without the need for multiple iteration and construction to obtain
CC humanised antibodies with suitable therapeutic properties. The antibody
CC has high affinity and low immunogenicity without need for comparing
CC framework sequences between non-human and human antibodies. This sequence
CC represents a human heavy chain variable region gene segment used in the
CC creation of humanised antibodies
XX
SQ Sequence 98 AA;

Alignment Scores:
Pred. No.: 0.00163 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 6 Gaps: 2

NOLAN463-2B.SEQ (1-84) x ABO27112 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

Search completed: August 4, 2005, 18:55:57
Job time : 93 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:44:26 ; Search time 22.25 Seconds
(without alignments)

563.642 Million cell updates/sec

Title: NOLAN463-2B.SEQ

Perfect score: 148

Sequence: 1 CGGGCGAGTCAGGTATTAG.....ACAGCCCGTCCTTCAAGGC 84

Scoring table:

| | | |
|-------------|-------------|-------------|
| BLOSUM62 | Xgapop 10.0 | Xgapext 0.1 |
| Ygapop 10.0 | Ygapext 0.1 | |
| Fgapop 6.0 | Fgapext 0.1 | |
| Delop 6.0 | Delext 0.1 | |

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO.spool.p/NOLAN08728463-2/runat_04082005_123945_22604/app_query.fasta_1.5
-DB=Issued Patents AA -QWTF=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCAL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN08728463-2 @CIGN 1.1 66 @runat_04082005_123945_22604 -NCPU=6 -ICPU=3
-NO.MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Issued Patents AA:*

| | |
|----|--|
| 1: | /cgn2_6/ptodata/1/iaa/5A.COMB.pap:* |
| 2: | /cgn2_6/ptodata/1/iaa/5B.COMB.pap:* |
| 3: | /cgn2_6/ptodata/1/iaa/6A.COMB.pap:* |
| 4: | /cgn2_6/ptodata/1/iaa/6B.COMB.pap:* |
| 5: | /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pap:* |
| 6: | /cgn2_6/ptodata/1/iaa/backfiles1.pap:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 103.4 | 69.9 | 98 | 1 | US-08-478-039-81 |
| 2 | 103.4 | 69.9 | 98 | 1 | US-08-476-349A-81 |
| 3 | 103.4 | 69.9 | 98 | 2 | US-08-665-202-33 |
| 4 | 103.4 | 69.9 | 98 | 4 | US-09-315-574-33 |
| 5 | 103.4 | 69.9 | 117 | 3 | US-08-545-809A-133 |
| 6 | 103.4 | 69.9 | 119 | 3 | US-09-025-769B-26 |
| 7 | 103.4 | 69.9 | 119 | 4 | US-09-490-070A-26 |
| 8 | 103.4 | 69.9 | 119 | 4 | US-09-490-153-26 |
| 9 | 103.4 | 69.9 | 119 | 4 | US-09-490-324-26 |
| 10 | 103.4 | 69.9 | 120 | 3 | US-09-025-769B-40 |
| 11 | 103.4 | 69.9 | 120 | 3 | US-09-025-769B-67 |
| 12 | 103.4 | 69.9 | 120 | 4 | US-09-490-070A-40 |

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 13 | 103.4 | 69.9 | 120 | 4 | US-09-490-070A-67 | Sequence 67, Appl |
| 14 | 103.4 | 69.9 | 120 | 4 | US-09-490-153-40 | Sequence 40, Appl |
| 15 | 103.4 | 69.9 | 120 | 4 | US-09-490-153-67 | Sequence 67, Appl |
| 16 | 103.4 | 69.9 | 120 | 4 | US-09-490-324-40 | Sequence 40, Appl |
| 17 | 103.4 | 69.9 | 120 | 4 | US-09-490-324-67 | Sequence 67, Appl |
| 18 | 103.2 | 69.7 | 111 | 4 | US-09-726-219A-171 | Sequence 171, App |
| 19 | 99.2 | 66.4 | 122 | 3 | US-08-983-607-30 | Sequence 30, Appl |
| 20 | 95 | 64.2 | 125 | 3 | US-08-665-202-44 | Sequence 44, Appl |
| 21 | 95 | 64.2 | 125 | 4 | US-09-315-574-44 | Sequence 44, Appl |
| 22 | 95 | 64.2 | 129 | 2 | US-08-665-202-32 | Sequence 32, Appl |
| 23 | 95 | 64.2 | 129 | 4 | US-09-315-574-32 | Sequence 32, Appl |
| 24 | 95 | 64.2 | 258 | 2 | US-08-665-202-5 | Sequence 5, Appl |
| 25 | 95 | 64.2 | 258 | 4 | US-09-315-574-5 | Sequence 5, Appl |
| 26 | 95 | 64.2 | 262 | 3 | US-09-069-821-4 | Sequence 4, Appl |
| 27 | 95 | 64.2 | 262 | 4 | US-09-956-086-4 | Sequence 4, Appl |
| 28 | 95 | 64.2 | 262 | 4 | US-09-956-087-4 | Sequence 4, Appl |
| 29 | 95 | 64.2 | 282 | 3 | US-09-420-592A-7 | Sequence 7, Appl |
| 30 | 95 | 64.2 | 282 | 4 | US-09-985-442-7 | Sequence 7, Appl |
| 31 | 95 | 64.2 | 282 | 4 | US-09-983-580-7 | Sequence 7, Appl |
| 32 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-48 | Sequence 48, Appl |
| 33 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-49 | Sequence 49, Appl |
| 34 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-50 | Sequence 50, Appl |
| 35 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-51 | Sequence 51, Appl |
| 36 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-52 | Sequence 52, Appl |
| 37 | 93.6 | 63.2 | 125 | 2 | US-08-665-202-57 | Sequence 57, Appl |
| 38 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-48 | Sequence 48, Appl |
| 39 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-49 | Sequence 49, Appl |
| 40 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-50 | Sequence 50, Appl |
| 41 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-51 | Sequence 51, Appl |
| 42 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-52 | Sequence 52, Appl |
| 43 | 93.6 | 63.2 | 125 | 4 | US-09-315-574-57 | Sequence 57, Appl |
| 44 | 93.2 | 63.0 | 88 | 4 | US-09-726-219A-172 | Sequence 172, App |
| 45 | 92.9 | 62.8 | 125 | 2 | US-08-665-202-47 | Sequence 47, Appl |

ALIGNMENTS

RESULT 1

US-08-478-039-81
; Sequence 81, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIORITY APPLICATION DATA:

```

, APPLICATION NUMBER: US 07/735,064
, FILING DATE: 25-JUL-1991
, ATTORNEY/AGENT INFORMATION:
, NAME: Teskin Esq., Robin L.
, REGISTRATION NUMBER: 35,030
, REFERENCE/DOCKET NUMBER: 012712-160
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 703-836-6620
, TELEFAX: 703-836-2021
, INFORMATION FOR SEQ ID NO: 81:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 98 amino acids
, TYPE: amino acid
, STRANDEDNESS: not relevant
, TOPOLOGY: not relevant
, MOLECULE TYPE: peptide
, ORIGINAL SOURCE:
, ORGANISM: Homo sapiens
, POSITION IN GENOME:
, CHROMOSOME/SEGMENT: VH5 consensus
US-08-478-039-81

```

| | | |
|------------------------|----------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 0.000271 | Length: |
| Score: | 103.40 | Matches: |
| Percent Similarity: | 45.28% | Conservative: |
| Best Local Similarity: | 43.40% | Mismatches: |
| Query Match: | 97.86% | Indels: |
| DB: | 1 | Gaps: |
| | | 2 |
| | | 26 |
| | | 3 |
| | | 1 |
| | | 23 |
| | | 98 |

NOLAN463-2B.SEO (1-84) x US-08-478-039-81 (1-98)

| | | | |
|----|----|--|----|
| QY | 3 | GGCGAGTCA-----GGGTATTACG----- | 21 |
| | | | |
| Db | 15 | GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyr-TrpIle | 34 |
| QY | 22 | -----AGCTGGTTAGGCATCATCTATCCTGG | 47 |
| | | | |
| Db | 34 | eGlyTyrValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleLeuTyr-ProGle | 54 |
| QY | 48 | TGACTCTGATACCACATACAGCCGCTCCTTCCAAGGC | 84 |
| Db | 54 | VAspSerAspThrArgTyrSerProSerPheGlnGly | 66 |

RESULT 2

```

US-08-476-349A-81
; Sequence 81, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995

```

```

, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/912,292
, FILING DATE: 10-JUL-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/856,281
, FILING DATE: 23-MAR-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/735,064
, FILING DATE: 25-JUL-1991
, ATTORNEY/AGENT INFORMATION:
, NAME: Teskin Beq., Robin L.
, REGISTRATION NUMBER: 35,030
, REFERENCE/DOCKET NUMBER: 012712-161
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 703-836-6620
, TELEFAX: 703-836-2021
, INFORMATION FOR SEQ ID NO: 81:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 98 amino acids
, TYPE: amino acid
, STRANDEDNESS: not relevant
, TOPOLOGY: not relevant
, MOLECULE TYPE: peptide
, ORIGINAL SOURCE:
, ORGANISM: Homo sapiens
, POSITION IN GENOME:
, CHROMOSOME/SEGMENT: VHS consensus
, US-08-476-349A-81

```

| | | |
|------------------------|----------|-----------------|
| Alignment Scores: | | |
| Pred. No.: | 0.000271 | 98 |
| Score: | 103.40 | 23 |
| Percent Similarity: | 45.28% | 1 |
| Best Local Similarity: | 43.40% | Conservative: 3 |
| Query Match: | 69.86% | Mismatches: 3 |
| DB: | 1 | Indels: 26 |
| | | Gaps: 2 |

NOI.AN463-2B.SEO (1-84) x IIS-08-476-349A-81 (1-98)

| | | | |
|----|----|---|----|
| Qy | 3 | GGCGAGTCA-----GGGTATTAGC----- | 21 |
| Db | 15 | GlyGluSerLeuLysIleSerCysLysGlyTyr-SerPheThrSerTyrTrpI | 34 |
| Qy | 22 | -----AGCTGGTTAGGCATCATCATCTTCCTGG | 47 |
| Db | 34 | eGlyTrpValArgLysMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG | 54 |
| Qy | 48 | TGACTCTGATACCACATACAGCCGCTCTTCCCAAGGC | 84 |
| Db | 54 | ValSerAspThrArcTyrSerProSerPheGlnGly | 66 |

RESULT 3

```

1  US-08-665-202-33
2  ; Sequence 33, Application US/08665202
3  ; Patent No. 5977322
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Marks, James D.
6  ; APPLICANT: Schier, Robert
7  ; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to Co
8  ; TITLE OF INVENTION: Tumor Antigens
9  ; NUMBER OF SEQUENCES: 141
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Townsend and Townsend and Crew LLP
12 ; STREET: Two Embarcadero Center, Eighth Floor
13 ; CITY: San Francisco
14 ; STATE: California
15 ; COUNTRY: USA
16 ; ZIP: 94111-3834
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/665,202
;; FILING DATE: 13-JUN-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunter, Tom
;; REGISTRATION NUMBER: 38,498
;; REFERENCE/DOCKET NUMBER: 02307E-061410
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-665-202-33

Alignment Scores:
Pred. No.: 0.000271 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-08-665-202-33 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 4
US-09-315-574-33
; Sequence 33, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99

;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/665,202
;; FILING DATE: 13-JUN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunter, Tom
;; REGISTRATION NUMBER: 38,498
;; REFERENCE/DOCKET NUMBER: 02307E-061411
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-315-574-33

Alignment Scores:
Pred. No.: 0.000271 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-315-574-33 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 5
US-08-545-809A-133
; Sequence 133, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-133

Alignment Scores:
Pred. No.: 0.000288 Length: 117
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 3 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-08-545-809A-133 (1-117)

Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 34 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 53
Qy 22 -----AGCTGGTTAGCCATCTATCTCTG 47
Db 53 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 73
Qy 48 TGACTCTGATACCATACAGCCGCTCTCCAGGC 84
Db 73 YAspSerAspThrArgTyrSerProSerPheGlnGly 85

RESULT 6
US-09-025-769B-26
; Sequence 26, Application US/09025769B
; Patent No. 6300084
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-26

Alignment Scores:
Pred. No.: 0.00029 Length: 119
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 3 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-26 (1-119)

Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
Qy 22 -----AGCTGGTTAGCCATCTATCTCTG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
Qy 48 TGACTCTGATACCATACAGCCGCTCTCCAGGC 84
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 7
US-09-490-070A-26
; Sequence 26, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-070A-26

Alignment Scores:
Pred. No.: 0.00029 Length: 119
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B-SEQ (1-84) x US-09-490-070A-26 (1-119)

Qy 3 GCGGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
Qy 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyLlelleTyrProGl 54
Qy 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 8

US-09-490-153-26
; Sequence 26, Application US/09490153
; Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-153-26

Alignment Scores:
Pred. No.: 0.00029 Length: 119
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B-SEQ (1-84) x US-09-490-153-26 (1-119)

Qy 3 GCGGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
Qy 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyLlelleTyrProGl 54
Qy 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 9

US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

```
;
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Alignment Scores:
Pred. No.: 0.00029 Length: 119
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-324-26 (1-119)
Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpIl 34
Qy 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54
Qy 48 TGACTCTGATACCATACATACAGCCGCTCTTCCAAAGGC 84
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 10
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-40

Alignment Scores:
Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 3 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-40 (1-120)
Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpIl 34
Qy 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleIleTyrProGl 54
Qy 48 TGACTCTGATACCATACATACAGCCGCTCTTCCAAAGGC 84
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 11
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```


US-09-025-769B-67

Alignment Scores:

Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 3 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-025-769B-67 (1-120)

QY 3 GGCGAGTCA-----GGGTATTAGC----- 21
DB 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
DB 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACCATACATACAGCCGCTCTTCCAAGGC 84
DB 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 12

US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/490,070A
APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-070A-40

Alignment Scores:

Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-070A-40 (1-120)

QY 3 GGCGAGTCA-----GGGTATTAGC----- 21
DB 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
DB 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACCATACATACAGCCGCTCTTCCAAGGC 84
DB 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 13

US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/490,070A
APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-490-070A-67

Alignment Scores:

Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23

Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-070A-67 (1-120)

Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
| | | | |
Db 15 GlyGlusSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpI1 34
Qy 22 -----AGCTGTTAGCCATCATCTATCCTGG 47
| | | | |
Db 34 eGlyTyrValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 54
Qy 48 TGACTCTGATACACATACAGCCCGCTCTTCCAAGGC 84
| | | | |
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 14

US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-153-40

Alignment Scores:
Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1

Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 4 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-09-490-153-40 (1-120)

Qy 3 GCGAGTCA-----GGGTATTAGC----- 21
| | | | |
Db 15 GlyGlusSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSeryTyrTrpI1 34
Qy 22 -----AGCTGTTAGCCATCATCTATCCTGG 47
| | | | |
Db 34 eGlyTyrValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 54
Qy 48 TGACTCTGATACACATACAGCCCGCTCTTCCAAGGC 84
| | | | |
Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 15

US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Alignment Scores:
Pred. No.: 0.00029 Length: 120
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26

```

DB:          4          Gaps:          2
NOLAN463-2B.SEQ (1-84) x US-09-490-153-67 (1-120)
QY   3  GCGAGTCA-----GGGTATTAGC----- 21
    |||||
Db  15  GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI 34
QY  22  -----AGCTGGTTAGCCATCATCTATCCTGG 47
    |||||
Db  34  eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG 54
QY  48  TGACTCTGATACACATACAGCCGCTCTCCAGGC 84
    |||||
Db  54  yAspSerAspThrArgTyrSerProSerPheGlnGly 66

```

Search completed: August 4, 2005, 19:04:16
Job time : 24.25 secs

THIS PAGE BLANK (USP 107)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: August 4, 2005, 19:01:38 ; Search time 78.75 Seconds
(without alignments)
832.849 Million cell updates/sec

Title: NOLAN463-2B.SEQ
Perfect score: 148
Sequence: 1 CGGGCGAGTCAGGTTATAG.....ACAGCCGCTCTTCCAGGC 84

Scoring table:
Xgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN08728463-2/runat_04082005_123947_22665/app_query.fasta_1.5
-DB=Published Applications AA -OPMT=faстан -SUFFIX=rapb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNIT8=bits -START=1 -END=-1 -MAIRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000
-USER=NOLAN08728463-2 @CIGN 1.1 260 @runat_04082005_123947_22665 -NCPU=6
-ICPU=3 -NO MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADs=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pcp.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Length | DB | ID | Description |
|------------|-------|---------|--------|----|--------------------|-------------------|
| 1 | 115 | 77.7 | 123 | 16 | US-10-466-242-49 | Sequence 49, Appl |
| 2 | 113.3 | 76.6 | 411 | 16 | US-10-769-144-12 | Sequence 12, Appl |
| 3 | 104.4 | 70.5 | 474 | 15 | US-10-291-265-284 | Sequence 284, App |
| 4 | 104.2 | 70.4 | 301 | 14 | US-10-002-631C-114 | Sequence 114, App |
| 5 | 103.4 | 69.9 | 98 | 9 | US-09-850-165-89 | Sequence 89, Appl |
| 6 | 103.4 | 69.9 | 98 | 14 | US-10-194-975-45 | Sequence 45, Appl |
| 7 | 103.4 | 69.9 | 98 | 14 | US-10-125-687-16 | Sequence 16, Appl |
| 8 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-6 | Sequence 6, Appl |
| 9 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-301 | Sequence 301, App |
| 10 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-312 | Sequence 302, App |
| 11 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-318 | Sequence 312, App |
| 12 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-318 | Sequence 318, App |
| 13 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-320 | Sequence 320, App |
| 14 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-336 | Sequence 336, App |
| 15 | 103.4 | 69.9 | 98 | 14 | US-10-041-860-367 | Sequence 367, App |
| 16 | 103.4 | 69.9 | 98 | 15 | US-10-308-817-88 | Sequence 88, Appl |
| 17 | 103.4 | 69.9 | 98 | 15 | US-10-032-037B-106 | Sequence 106, App |
| 18 | 103.4 | 69.9 | 98 | 15 | US-10-032-037B-107 | Sequence 107, App |
| 19 | 103.4 | 69.9 | 98 | 15 | US-10-032-037B-108 | Sequence 108, App |
| 20 | 103.4 | 69.9 | 98 | 15 | US-10-029-988B-106 | Sequence 106, App |
| 21 | 103.4 | 69.9 | 98 | 15 | US-10-029-988B-107 | Sequence 107, App |
| 22 | 103.4 | 69.9 | 98 | 15 | US-10-029-988B-108 | Sequence 108, App |
| 23 | 103.4 | 69.9 | 98 | 15 | US-10-032-423A-106 | Sequence 106, App |
| 24 | 103.4 | 69.9 | 98 | 15 | US-10-032-423A-107 | Sequence 107, App |
| 25 | 103.4 | 69.9 | 98 | 15 | US-10-032-423A-108 | Sequence 108, App |
| 26 | 103.4 | 69.9 | 98 | 15 | US-10-453-698-88 | Sequence 88, Appl |
| 27 | 103.4 | 69.9 | 98 | 15 | US-10-029-926B-106 | Sequence 106, App |
| 28 | 103.4 | 69.9 | 98 | 15 | US-10-029-926B-107 | Sequence 107, App |
| 29 | 103.4 | 69.9 | 98 | 15 | US-10-029-926B-108 | Sequence 108, App |
| 30 | 103.4 | 69.9 | 98 | 16 | US-10-379-392-53 | Sequence 53, Appl |
| 31 | 103.4 | 69.9 | 98 | 16 | US-10-796-144-30 | Sequence 30, Appl |
| 32 | 103.4 | 69.9 | 98 | 18 | US-10-996-191-16 | Sequence 16, Appl |
| 33 | 103.4 | 69.9 | 109 | 16 | US-10-800-197-144 | Sequence 144, App |
| 34 | 103.4 | 69.9 | 109 | 16 | US-10-800-197-145 | Sequence 145, App |
| 35 | 103.4 | 69.9 | 109 | 16 | US-10-800-197-146 | Sequence 146, App |
| 36 | 103.4 | 69.9 | 109 | 17 | US-10-727-155-283 | Sequence 283, App |
| 37 | 103.4 | 69.9 | 109 | 17 | US-10-727-155-291 | Sequence 291, App |
| 38 | 103.4 | 69.9 | 110 | 17 | US-10-726-332-217 | Sequence 217, App |
| 39 | 103.4 | 69.9 | 116 | 17 | US-10-727-155-100 | Sequence 100, App |
| 40 | 103.4 | 69.9 | 117 | 17 | US-10-684-957-10 | Sequence 10, Appl |
| 41 | 103.4 | 69.9 | 117 | 17 | US-10-684-957-30 | Sequence 30, Appl |
| 42 | 103.4 | 69.9 | 117 | 17 | US-10-726-332-9 | Sequence 9, Appl |
| 43 | 103.4 | 69.9 | 117 | 17 | US-10-726-332-138 | Sequence 138, App |
| 44 | 103.4 | 69.9 | 117 | 17 | US-10-726-332-144 | Sequence 144, App |
| 45 | 103.4 | 69.9 | 118 | 17 | US-10-726-332-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-10-466-242-49
; Sequence 49, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466.242
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens

```
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(123)
; OTHER INFORMATION: Clone 2b:7 VH
US-10-466-242-49

Alignment Scores:
Pred. No.: 0.000145 Length: 123
Score: 115.00 Matches: 23
Percent Similarity: 55.32% Conservative: 3
Best Local Similarity: 48.94% Mismatches: 1
Query Match: 77.70% Indels: 20
DB: 16 Gaps: 1

NOLAN463-2B.SEQ (1-84) x US-10-466-242-49 (1-123)

QY 1 CGGCGAGT----- 9
Db 25 ArgAlaSerGlyTyrSerPheSerLeuPheTrpValAlaTrpValArgGlnMetProGly 44
QY 10 CAGGTATTAGCAGCTGTTAGCCATCATCTCTGCTGACTCTGATACCATACAGC 69
Db 45 GlnGlyLeu---GluTrpMetAlaIleIleTyrProGlyAspSerAspThrThrTyrSer 63
QY 70 CCGTCCTTCCAAAGC 84
Db 64 ProSerPheGlnGly 68

RESULT 2
US-10-769-144-12
; Sequence 12, Application US/10769144
; Publication No. US20040248215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Endres, Michael
; APPLICANT: He, Lizhen
; APPLICANT: Ramakrishna, Venky
; TITLE OF INVENTION: ANTIBODY VACCINE CONJUGATES AND USES
; FILE REFERENCE: MX1-301
; CURRENT APPLICATION NUMBER: US/10/769,144
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: 60/443979
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-144-12

Alignment Scores:
Pred. No.: 0.000293 Length: 411
Score: 113.30 Matches: 26
Percent Similarity: 15.78% Conservative: 0
Best Local Similarity: 15.78% Mismatches: 2
Query Match: 76.55% Indels: 137
DB: 16 Gaps: 1

NOLAN463-2B.SEQ (1-84) x US-10-769-144-12 (1-411)

QY 1 CGGCGAGTCAGGTATTAGCAGCTGGTTAGCC----- 33
Db 43 ArgAlaSerGlnGlyIleSerArgTrpLeuAlaTrpTyrGlnGlnLysProGluLysAla 62
QY 33 ----- 33
Db 63 ProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 82
QY 33 ----- 33
Db 83 GlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnProGluAspPhe 102

; RESULT 3
US-10-291-265-284
; Sequence 284, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR FILING DATE: 09/491,404
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 284
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-284

Alignment Scores:
Pred. No.: 0.00333 Length: 474
Score: 104.40 Matches: 23
Percent Similarity: 47.17% Conservative: 2
Best Local Similarity: 43.40% Mismatches: 2
Query Match: 70.54% Indels: 26
DB: 15 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-291-265-284 (1-474)

QY 3 GCGCAGTCA-----GGGTATTAGC----- 21
Db 34 GlyGluSerValLysIleSerCysLysGlySerGlyTyr-SerPheSerAspTyrTrpVa 53
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 53 LalaTrpValArgGlnSerProAspLysGlyLeuAlaTrpMetGlyIleIleTyrProGl 73
QY 48 TGACTCTGATACCATACAGCCCGTCTCTCCNAGGC 84
Db 73 yAspSerAspThrArgTyrSerProSerPheGlnGly 85
```



```
; Sequence 16, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-16

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-125-687-16 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
D 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
D 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
D 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 8
US-10-041-860-6
; Sequence 6, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-6

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-6 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
D 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
D 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
D 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 9
US-10-041-860-301
; Sequence 301, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-301

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-301 (1-98)

QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
D 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
D 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
D 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 10
US-10-041-860-302
; Sequence 302, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
```


APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 302
LENGTH: 98
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: 23
OTHER INFORMATION: Xaa = Any Amino Acid
FEATURE:
NAME/KEY: VARIANT
LOCATION: 23
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-302

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-302 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCys**GlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyr-ProG1 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 11
US-10-041-860-312
; Sequence 312, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-312

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23

Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2
NOLAN463-2B.SEQ (1-84) x US-10-041-860-312 (1-98)
QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyr-ProG1 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 12
US-10-041-860-318
; Sequence 318, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-318

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-318 (1-98)
QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyr-ProG1 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 13
US-10-041-860-320
; Sequence 320, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.

```
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 68
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 68
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-10-041-860-320

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-320 (1-98)
QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 14
US-10-041-860-336
; Sequence 336, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-367

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-367 (1-98)
QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 15
US-10-041-860-336
; Sequence 367, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-367

Alignment Scores:
Pred. No.: 0.00316 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 14 Gaps: 2

NOLAN463-2B.SEQ (1-84) x US-10-041-860-336 (1-98)
QY 3 GCGAGTCA-----GGGTATTAGC----- 21
Db 15 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpIl 34
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 54
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 54 yAspSerAspThrArgTyrSerProSerPheGlnGly 66
```

Search completed: August 4, 2005, 19:30:18
Job time : 79.75 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 18:42:17 ; Search time 17.75 Seconds
(without alignments)
910.671 Million cell updates/sec

Title: NOLAN463-2B.SEQ
Perfect score: 148
Sequence: 1 CGGGCCAGTCAGGCTATTAG.....ACAGCCCGCTCTCCAGGC 84

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O/cn2.1/USPTO.spool.p/NOLAN08728463-2/runat.04082005.123944.22592/app_query.fasta.1.5
-DB=pir -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN08728463-2 @CGN 1.1.77 @runat.04082005.123944.22592 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOPE=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 108.7 | 73.4 | 102 | 2 | PHI277 |
| 2 | 106.7 | 72.1 | 127 | 2 | PHI409 |
| 3 | 103.4 | 69.9 | 98 | 2 | PHI274 |
| 4 | 103.4 | 69.9 | 98 | 2 | S26907 |
| 5 | 103.4 | 69.9 | 101 | 2 | S12428 |
| 6 | 103.4 | 69.9 | 101 | 2 | S12424 |
| 7 | 103.4 | 69.9 | 102 | 2 | PHI266 |
| 8 | 103.4 | 69.9 | 102 | 2 | PHI279 |
| 9 | 103.4 | 69.9 | 102 | 2 | PHI281 |
| 10 | 103.4 | 69.9 | 102 | 2 | PHI284 |
| 11 | 103.4 | 69.9 | 102 | 2 | PHI272 |
| 12 | 103.4 | 69.9 | 102 | 2 | PHI282 |
| 13 | 103.4 | 69.9 | 102 | 2 | PHI258 |
| 14 | 103.4 | 69.9 | 102 | 2 | PHI264 |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 15 | 103.4 | 69.9 | 102 | 2 | PHI259 | Ig heavy chain V r |
| 16 | 103.4 | 69.9 | 102 | 2 | PHI273 | Ig heavy chain V r |
| 17 | 103.4 | 69.9 | 102 | 2 | PHI249 | Ig heavy chain V r |
| 18 | 103.4 | 69.9 | 102 | 2 | PHI271 | Ig heavy chain V r |
| 19 | 103.4 | 69.9 | 102 | 2 | PHI278 | Ig heavy chain V r |
| 20 | 103.4 | 69.9 | 113 | 2 | PHI428 | Ig heavy chain V r |
| 21 | 103.4 | 69.9 | 115 | 2 | PHI557 | Ig heavy chain V r |
| 22 | 103.4 | 69.9 | 117 | 2 | A28846 | Ig heavy chain pre |
| 23 | 103.4 | 69.9 | 123 | 2 | PHI423 | Ig heavy chain V r |
| 24 | 103.4 | 69.9 | 123 | 2 | S38492 | Ig heavy chain - h |
| 25 | 103.4 | 69.9 | 123 | 2 | C36006 | Ig heavy chain V r |
| 26 | 103.4 | 69.9 | 127 | 2 | PHI414 | Ig heavy chain V r |
| 27 | 103.4 | 69.9 | 127 | 2 | PHI411 | Ig heavy chain V r |
| 28 | 103.4 | 69.9 | 128 | 2 | S16685 | Ig heavy chain V r |
| 29 | 103.4 | 69.9 | 134 | 2 | PHI422 | Ig heavy chain V r |
| 30 | 103.4 | 69.9 | 136 | 2 | A49047 | Ig heavy chain V r |
| 31 | 103.4 | 69.9 | 139 | 2 | PHI558 | Ig heavy chain V r |
| 32 | 103.2 | 69.7 | 102 | 2 | PHI267 | Ig heavy chain V r |
| 33 | 103.2 | 69.7 | 102 | 2 | PHI280 | Ig heavy chain V r |
| 34 | 103.2 | 69.7 | 104 | 2 | B36006 | Ig heavy chain V r |
| 35 | 103.2 | 69.7 | 117 | 2 | S19670 | Ig heavy chain V r |
| 36 | 103.2 | 69.7 | 136 | 2 | PHI559 | Ig heavy chain V r |
| 37 | 102.4 | 69.2 | 98 | 2 | PHI077 | Ig heavy chain V r |
| 38 | 101 | 68.2 | 102 | 2 | PHI248 | Ig heavy chain V r |
| 39 | 100.4 | 67.8 | 102 | 2 | PHI252 | Ig heavy chain V r |
| 40 | 99.4 | 67.2 | 123 | 2 | PHI413 | Ig heavy chain V r |
| 41 | 98.4 | 66.5 | 102 | 2 | PHI265 | Ig heavy chain V r |
| 42 | 98.3 | 66.4 | 126 | 2 | PHI416 | Ig heavy chain V r |
| 43 | 98.3 | 66.4 | 126 | 2 | PHI419 | Ig heavy chain V r |
| 44 | 98.2 | 66.4 | 86 | 2 | S12580 | Ig heavy chain V r |
| 45 | 97.4 | 65.8 | 102 | 2 | PHI247 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

PHI277
Ig heavy chain V region (clone PBL8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PHI277
R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
A:Reference number: PHI232; MUID:93018822; PMID:1402653
A:Accession: PHI277
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.06e-05 Length: 102
Score: 108.70 Matches: 19
Percent Similarity: 76.67% Conservative: 4
Best Local Similarity: 63.33% Mismatches: 4
Query Match: 73.45% Indels: 3
DB: 2 Gaps: 0

NOLAN463-2B.SEQ (1-84) x PHI277 (1-102)

QY 1 CGGGCGAGTCAGGCTATTAGCAGCTGGTTAGCCATCATCTCTGGTGACTCTGATACC 60
Db 44 LysAlaGlyLysGlyLeu---GluTrpMetGlyIleIleIleTyProGlyAAspSerAspThr 62
QY 61 ACATACAGCCGCTCTTCCAAGGC 84

Db 63 ArgTyrSerProSerPheGlnGly 70

RESULT 2

PHI409

Ig heavy chain V region (clone PI-51) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1409

R:Van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1409

A:Molecule type: mRNA

A:Residues: 1-127 <VAN>

A:Experimental source: PBMC

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 5.59e-05 Length: 127
Score: 106.70 Matches: 19
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 63.33% Mismatches: 5
Query Match: 72.09% Indels: 3
DB: 2 Gaps: 0

NOLAN463-2B.SEQ (1-84) x PH1409 (1-127)

QY 1 CGGCGAGTCAGGTATTAGCAGCTGTTAGCCATCATCTCTGGTGACCTCATACC 60

Db 40 ArgProGlyLysGlyLeu---GluTrpMetGlyIleIleTy:ProGlyAspSerAspThr 58

QY 61 ACATACAGCCGCTCTTCCCAAGC 84

Db 59 ArgTyrSerProSerPheGlnGly 66

RESULT 3

PH1274

Ig heavy chain V region (clone PBL5) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1274

R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1274

A:Molecule type: DNA

A:Residues: 1-98 <CAI>

A:Experimental source: adult PBL

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 0.000145 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1274 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21

Db 19 GlyGluSerLeuLysIleSerCysGlySerGlyTyr-SerPheThrSerTyrTrpI 38

QY 22 -----AGCTGTTAGCCATCATCTCTG 47

Db 38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTy:ProG 50

QY 48 TGACTCTGATACACATACAGCCGCTCTTCCCAAGC 84

Db 58 YAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 4

S26907

Ig heavy chain V region (DP-73) - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26907

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26907

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <OM>

A:Cross-references: EMBL:Z12373; NID:932965; PIDN:CAA78243.1; PID:932966

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 98
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x S26907 (1-98)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21

Db 15 GlyGluSerLeuLysIleSerCysGlySerGlyTyr-SerPheThrSerTyrTrpI 34

QY 22 -----AGCTGTTAGCCATCATCTCTG 47

Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTy:ProG 54

QY 48 TGACTCTGATACACATACAGCCGCTCTTCCCAAGC 84

Db 54 YAspSerAspThrArgTyrSerProSerPheGlnGly 66

RESULT 5

S12428

Ig heavy chain V region (5JB) - human

C:Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S12428

R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.

EMBO J. 8, 3741-3748, 1989

A:Title: The smaller human V(H) gene families display remarkably little polymorphism.

A:Reference number: S09421; MUID:90059975; PMID:2511001

A:Accession: S12428

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-101 <SAN>

A:Cross-references: EMBL:X56367

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:18-101/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 101
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x S12428 (1-101)

QY 3 GCGAGTCA-----GGGTATTAGC----- 21

Db 15 GlyGluSerLeuLysIleSerCysGlySerGlyTyr-SerPheThrSerTyrTrpI 34

QY 22 -----AGCTGTTAGCCATCATCTCTG 47

Db 34 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTy:ProG 54

QY 48 TGACTCTGATACACATACAGCCGCTCTTCCCAAGC 84

Db 58 YAspSerAspThrArgTyrSerProSerPheGlnGly 70

Db 18 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 37
 QY 22 -----ACGTGGTTAGCCATCATCTATCTCTGG 47
 Db 37 eGlyTTPValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 57
 QY 48 TGACTCTGATACCATACAGCCCGTCTTCCAGGC 84
 Db 57 yAspSerAspThrArgTyrSerProSerPheGlnGly 69
 RESULT 6
 S12424
 Ig heavy chain V region (S) - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text change 03-Aug-1998
 C:Accession: S12424; S12425; S12426; S12427; S12429; S12432
 R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
 EMBL J. 8. 3741-3748, 1989
 A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
 A:Reference number: S09421; MUID:90059975; PMID:2511001
 A:Accession: S12424
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA1>
 A:Cross-references: EMBL:X56372
 A:Experimental source: clones 5AU; 5BLK; 5CH; 5CW; 5LB; 5TT
 A:Accession: S12425
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA2>
 A:Cross-references: EMBL:X56373
 A:Accession: S12426
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA3>
 A:Cross-references: EMBL:X56370
 A:Accession: S12427
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA4>
 A:Cross-references: EMBL:X56368
 A:Accession: S12429
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA5>
 A:Cross-references: EMBL:X56369
 A:Accession: S12432
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101 <SA6>
 A:Cross-references: EMBL:X56371
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:18-101/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 0.000145 Length: 101
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 2 Gaps: 2
 NOLAN463-2B.SEQ (1-84) x S12424 (1-101)
 QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
 Db 18 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 37
 QY 22 -----ACGTGGTTAGCCATCATCTATCTCTGG 47
 Db 37 eGlyTTPValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 57

QY 48 TGACTCTGATACCATACAGCCCGTCTTCCAGGC 84
 Db 57 yAspSerAspThrArgTyrSerProSerPheGlnGly 69
 RESULT 7
 PH1266
 Ig heavy chain V region (clone VERGS) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1266
 R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
 A:Reference number: PH1232; MUID:93018822; PMID:1402653
 A:Accession: PH1266
 A:Molecule type: mRNA
 A:Residues: 1-102 <CAI>
 A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 0.000145 Length: 102
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 2 Gaps: 2
 NOLAN463-2B.SEQ (1-84) x PH1266 (1-102)
 QY 3 GCGGAGTCA-----GGGTATTAGC----- 21
 Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 38
 QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
 Db 38 eGlyTTPValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 58
 QY 48 TGACTCTGATACCATACAGCCCGTCTTCCAGGC 84
 Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
 RESULT 8
 PH1279
 Ig heavy chain V region (clones CLL11, CORD3, CORD4, CORD8, CORD9, CD+1, CD+3, CD+4, CD
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1279
 R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
 J. Exp. Med. 176, 1073-1081, 1992
 A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chro
 A:Reference number: PH1232; MUID:93018822; PMID:1402653
 A:Accession: PH1279
 A:Molecule type: DNA
 A:Residues: 1-102 <CAI>
 A:Experimental source: adult PBL
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-102/Domain: immunoglobulin homology <IMM>
 Alignment Scores:
 Pred. No.: 0.000145 Length: 102
 Score: 103.40 Matches: 23
 Percent Similarity: 45.28% Conservative: 1
 Best Local Similarity: 43.40% Mismatches: 3
 Query Match: 69.86% Indels: 26
 DB: 2 Gaps: 2
 NOLAN463-2B.SEQ (1-84) x PH1279 (1-102)
 QY 3 GCGGAGTCA-----GGGTATTAGC----- 21

```
|||||
19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 38
QY 22 -----AGCTGGTTAGCCATCACTATCCTGG 47
Db 38 eGlyTrpValArgInMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 58
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70

RESULT 9
PH1281
Ig heavy chain V region (clone PBL12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1281
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1281
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1281 (1-102)
QY 3 GCGCAGTGCA-----GGGTATTAGC----- 21
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 38
QY 22 -----AGCTGGTTAGCCATCACTATCCTGG 47
Db 38 eGlyTrpValArgInMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 58

RESULT 10
PH1244
Ig heavy chain V region (clone CORD2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1244
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1244
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: cord blood B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
```

```
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1244 (1-102)
QY 3 GCGCAGTGCA-----GGGTATTAGC----- 21
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI1 38
QY 22 -----AGCTGGTTAGCCATCACTATCCTGG 47
Db 38 eGlyTrpValArgInMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 58

RESULT 11
PH1272
Ig heavy chain V region (clone PBL3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1272
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1272
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1272 (1-102)
QY 3 GCGCAGTGCA-----GGGTATTAGC----- 21
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrThrTyrTrpI1 38
QY 22 -----AGCTGGTTAGCCATCACTATCCTGG 47
Db 38 eAlaTrpValArgInMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProG1 58

RESULT 12
PH1282
Ig heavy chain V region (clone PBL13) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1282
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1282
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: adult PBL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```


C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1282 (1-102)

```
QY 3 GCGAGTCA-----GGGTATTAGC-----21
  |||||
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI 38
  |||||
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
  |||||
Db 38 eGlyTrpValArgGlnThrProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58
  |||||
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
  |||||
Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
  |||||
```

RESULT 13

PH1258
Ig heavy chain V region (clone CD-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1258
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID: 93018822; PMID: 1402653
A:Accession: PH1258
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: cord blood B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1258 (1-102)

```
QY 3 GCGAGTCA-----GGGTATTAGC-----21
  |||||
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheIleAsnTyrTrpI 38
  |||||
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
  |||||
Db 38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58
  |||||
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
  |||||
Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
  |||||
```

RESULT 14

PH1264
Ig heavy chain V region (clone VERG3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1264
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID: 93018822; PMID: 1402653
A:Accession: PH1264
A:Molecule type: mRNA
A:Residues: 1-102 <CAI>
A:Experimental source: EBV-transformed CD5+ B cell [from adult PBL]
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1264 (1-102)

```
QY 3 GCGAGTCA-----GGGTATTAGC-----21
  |||||
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheSerSerTyrTrpI 38
  |||||
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
  |||||
Db 38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58
  |||||
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
  |||||
Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
  |||||
```

RESULT 15

PH1259
Ig heavy chain V region (clone CD-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1259
R: Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chrom
A:Reference number: PH1232; MUID: 93018822; PMID: 1402653
A:Accession: PH1259
A:Molecule type: DNA
A:Residues: 1-102 <CAI>
A:Experimental source: cord blood B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000145 Length: 102
Score: 103.40 Matches: 23
Percent Similarity: 45.28% Conservative: 1
Best Local Similarity: 43.40% Mismatches: 3
Query Match: 69.86% Indels: 26
DB: 2 Gaps: 2

NOLAN463-2B.SEQ (1-84) x PH1259 (1-102)

```
QY 3 GCGAGTCA-----GGGTATTAGC-----21
  |||||
Db 19 GlyGluSerLeuLysIleSerCysLysGlySerGlyTyr-SerPheThrSerTyrTrpI 38
  |||||
QY 22 -----AGCTGGTTAGCCATCATCTATCTCTGG 47
  |||||
Db 38 eGlyTrpValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGl 58
  |||||
QY 48 TGACTCTGATACACATACAGCCGCTCTTCCAAGGC 84
  |||||
Db 58 yAspSerAspThrArgTyrSerProSerPheGlnGly 70
  |||||
```

Search completed: August 4, 2005, 19:02:37
Job time : 18.75 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.
 OM nucleic - protein search, using frame_plus_n2p model
 Run on: August 4, 2005, 18:23:15 ; Search time 80.75 Seconds
 (without alignments)
 1065.378 Million cell updates/sec

Title: NOLAN463-2B.SEQ
 Perfect score: 148
 Sequence: 1 CGGGCGAGTCAGGGTATTAG.....ACAGCCCGCTCTTCAAGGC 84

Scoring table:
 BLOSUM62
 Xgapop 10.0, Xgapext 0.1
 Ygapop 10.0, Ygapext 0.1
 Fgapop 6.0, Fgapext 0.1
 Delop 6.0, Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
 -MODEL=frame+n2p.model -DEV=xlp
 -O=/cgn2.1/USPTO.spool.p/NOLAN08728463-2/runat.04082005.123944.22581/app_query.fasta_1.5
 -DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -DOPEXT=0
 -UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
 -USER=NOLAN08728463-2 @CGN 1.1 305 @runat.04082005.123944.22581 -NCPU=6
 -ICPU=3 -NO MMAP -LARGEQUERY -NOSCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : UniProt 03.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 84.7 | 57.2 | 118 | Q921C4 | Q921C4 mus musculus |
| 2 | 77.7 | 52.5 | 474 | Q8R3H6 | Q8R3H6 mus musculus |
| 3 | 76.7 | 51.8 | 111 | Q9D9B8 | Q9D9B8 mus musculus |
| 4 | 75.7 | 51.1 | 614 | Q7TMT6 | Q7TMT6 mus musculus |
| 5 | 74.7 | 50.5 | 117 | HV06 MOUSE | P01750 mus musculus |
| 6 | 74.7 | 50.5 | 117 | HV052 MOUSE | P06327 mus musculus |
| 7 | 73.7 | 49.8 | 110 | Q9JL83 | Q9JL83 mus musculus |
| 8 | 73.7 | 49.8 | 481 | Q91WT1 | Q91WT1 mus musculus |
| 9 | 72.7 | 49.1 | 464 | Q6PF95 | Q6PF95 mus musculus |
| 10 | 71.7 | 48.4 | 463 | Q99LCA | Q99LCA mus musculus |
| 11 | 68.2 | 46.1 | 125 | HV1F HUMAN | P06326 homo sapien |
| 12 | 67.7 | 45.7 | 117 | HV05 MOUSE | P01749 mus musculus |
| 13 | 66.7 | 45.1 | 143 | Q91V67 | Q91V67 mus musculus |
| 14 | 65.5 | 44.3 | 236 | Q6GMX8 | Q6GMX8 homo sapien |
| 15 | 64.7 | 43.7 | 136 | Q7TPE3 | Q7TPE3 mus musculus |
| 16 | 63.8 | 43.1 | 370 | Q7N4R1 | Q7N4R1 photorhabdu |

| | | | | | | |
|------|------|------|------|---|------------|---------------------|
| 17 | 63.7 | 43.0 | 121 | 2 | Q9UL96 | Q9UL96 homo sapien |
| 18 | 63.7 | 43.0 | 143 | 2 | Q924Q0 | Q924Q0 mus musculus |
| 19 | 62.7 | 42.4 | 147 | 2 | Q925S3 | Q925S3 mus musculus |
| 20 | 62.5 | 42.2 | 1680 | 2 | Q9P1Z9 | Q9P1Z9 homo sapien |
| c 21 | 62.3 | 39.0 | 295 | 2 | Q8Z1R4 | Q8Z1R4 salmonella |
| c 22 | 62.3 | 39.0 | 295 | 2 | Q8ZKG0 | Q8ZKG0 salmonella |
| 23 | 62 | 41.9 | 98 | 2 | Q8B6V3 | Q8B6V3 oryctolagus |
| 24 | 62 | 41.9 | 98 | 2 | Q8B6W5 | Q8B6W5 oryctolagus |
| 25 | 62 | 41.9 | 99 | 2 | Q8B6S4 | Q8B6S4 oryctolagus |
| 26 | 62 | 41.9 | 99 | 2 | Q8B6S7 | Q8B6S7 oryctolagus |
| 27 | 61.7 | 41.7 | 117 | 1 | HV1B HUMAN | P01743 homo sapien |
| 28 | 61.7 | 41.7 | 124 | 2 | Q9UL92 | Q9UL92 homo sapien |
| c 29 | 61.6 | 38.5 | 302 | 2 | Q919C3 | Q919C3 anguilla an |
| 30 | 61.1 | 41.3 | 4335 | 2 | Q6NA45 | Q6NA45 rhodopseuo |
| 31 | 60.7 | 41.0 | 143 | 2 | Q924P9 | Q924P9 mus musculus |
| 32 | 60.7 | 41.0 | 330 | 2 | Q91KW0 | Q91KW0 streptomyce |
| 33 | 60.7 | 41.0 | 481 | 2 | Q91WT3 | Q91WT3 mus musculus |
| 34 | 60.7 | 41.0 | 1189 | 2 | Q8NSU0 | Q8NSU0 corynebacte |
| 35 | 60.7 | 41.0 | 1208 | 2 | Q6M7I4 | Q6M7I4 corynebacte |
| 36 | 60.6 | 40.9 | 733 | 2 | Q658I3 | Q658I3 oryza sativ |
| 37 | 60.5 | 40.9 | 117 | 1 | KV1I HUMAN | P01601 homo sapien |
| 38 | 60.2 | 40.7 | 390 | 2 | Q7S6A9 | Q7S6A9 neurospora |
| 39 | 60.1 | 40.6 | 763 | 2 | Q7Q5E3 | Q7Q5E3 anopheles g |
| 40 | 60 | 40.5 | 537 | 2 | Q6GNX4 | Q6GNX4 xenopus lae |
| c 41 | 59.8 | 37.4 | 524 | 2 | Q6ZM46 | Q6ZM46 brachydanio |
| 42 | 59.7 | 40.3 | 120 | 1 | HV03 MOUSE | P01747 mus musculus |
| 43 | 59.7 | 40.3 | 487 | 2 | Q65ZL2 | Q65ZL2 mus sp. fv/ |
| 44 | 59.5 | 40.2 | 107 | 1 | KV1J HUMAN | P01596 homo sapien |
| 45 | 59.5 | 40.2 | 117 | 1 | KV1J_HUMAN | P01602 homo sapien |

ALIGNMENTS

RESULT 1
 Q921C4 PRELIMINARY; PRT; 118 AA.
 ID Q921C4;
 AC Q921C4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c;
 RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.A., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells";
 RL MOL. Immunol. 34:441-452(1997).
 DR HSSP; P01751; INQB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 13036 MW; 90EECS59D31EC4FC CRC64;

Alignment Scores:
 Pred. No.: 0.141 Length: 118
 Score: 84.70 Matches: 14
 Percent Similarity: 63.33% Conservative: 5
 Best Local Similarity: 46.87% Mismatches: 8
 Query Match: 57.23% Indels: 3
 DB: 2 Gaps: 0

```
NOLAN463-2B_SEQ (1-84) x Q9Z1C4 (1-118)
QY 1 CGGGCGAGTCAGGTATTAGCAGCTGGTTAGCCATCATCTATCTCGTGGTACTCTGATACC 60
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 ArgProGlyGlnGlyLeu---GluTrpIleGlyAlaIleTyrProGlyAspGlyAspThr 58
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACATACAGCCCGCTCTCCAGGC 84
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 SerTyrThrGlnLysPheArgGly 66
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
Q9Z1C4 PRELIMINARY; PRT; 474 AA.
AC Q9Z1C4 (1-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AU044919 protein.
GN Name=AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR HSP; P01869; ICL7.
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CycC_heme_BS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Alignment Scores:
Pred. No.: 1.4 Length: 474
Score: 77.70 Matches: 14
Percent Similarity: 60.00% Conservative: 4
Best Local Similarity: 46.67% Mismatches: 9
Query Match: 52.50% Indels: 3
```

```
DB: 2 Gaps: 0
NOLAN463-2B_SEQ (1-84) x Q8R3H6 (1-474)
QY 1 CGGGCGAGTCAGGTATTAGCAGCTGGTTAGCCATCATCTATCTCGTGGTACTCTGATACC 60
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 ArgProGlyLysGlyLeu---GluTrpIleGlyArgIlePheProGlyAspGlyAspThr 77
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ACATACAGCCCGCTCTCCAGGC 84
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 HisTyrSerGlyLysPheGlnGly 85
   ||| |||||:|:| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
Q8R3H6 PRELIMINARY; PRT; 111 AA.
AC Q8R3H6 (1-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:170010101 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
```

```

RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS003596; IG_v.
DR PROSITE; PS0835; IG LIKE; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Alignment Scores:
Pred. No.: 1.49 Length: 111
Score: 76.70 Matches: 13
Percent Similarity: 60.00% Conservative: 5
Best Local Similarity: 43.33% Mismatches: 9
Query Match: 51.82% Indels: 3
DB: 2 Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q9D9B8 (1-111)
Qy 1 CGGCGAGTCAGGTATTAGCAGCTGTTAGCCATCATCTATCTCTGTCGATCTGTATACC 60
Db 46 ArgProGlyLysGlyLeu---GlutPileGlyArgIleTyProGlyAspGlyAspThr 64
Qy 61 ACATACAGCCCGCTCTTCCCAAGGC 84
Db 65 AsnTyraenGlyLysPheLysGly 72

RESULT 4
Q7TWT6 PRELIMINARY; PRT; 614 AA.
AC Q7TWT6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA "Generation and initial analysis of more than 15,000 full-length human

```

```

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAHS3409.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124P89 CRC64;

Alignment Scores:
Pred. No.: 2.64 Length: 614
Score: 75.70 Matches: 12
Percent Similarity: 60.00% Conservative: 6
Best Local Similarity: 40.00% Mismatches: 9
Query Match: 51.15% Indels: 3
DB: 2 Gaps: 0

NOLAN463-2B.SEQ (1-84) x Q7TWT6 (1-614)
Qy 1 CGGCGAGTCAGGTATTAGCAGCTGTTAGCCATCATCTATCTCTGTCGATCTGTATACC 60
Db 59 ArgProGlyLysGlyLeu---GlutPileGlyArgValTyProGlyAspGlyAspThr 77
Qy 61 ACATACAGCCCGCTCTTCCCAAGGC 84
Db 78 AsnTyraenGlyLysPheLysGly 85

RESULT 5
HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
CC Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NPB antibodies.
DR PTR; A02032; HVMS02.
DR PDB; 1QNZ; NMR; H=20-117.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS003596; IG LIKE; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 19 Ig heavy chain V region 102.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.

```


DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DI Igh-VJ558 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX STRAIN=C2B6 II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013490; AAH13490.1; -;
 DR HSSP; P01751; IAGW.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
 Alignment Scores:
 Pred. No.: 4.58 Length: 481
 Score: 73.70 Matches: 13
 Percent Similarity: 60.00% Conservative: 5
 Best Local Similarity: 43.33% Mismatches: 9
 Query Match: 49.80% Indels: 3
 DB: 2 Gaps: 0
 NOLAN463-2B.SEQ (1-84) x Q91WT1 (1-481)
 Qy 1 CGGGCGAGTCAGGTATTAGCAGCTGGTATGCCATCTCTCTCTGGTACTGTGATACC 60
 Db 59 ArgProGlyGinglyLeu---ValTrpIleGlyTrpIleTyProGlyAspGlyAsnThr 77
 Qy 61 ACATACACCCGCTCTCTCCCAAGGC 84
 Db 78 LysTyraenGluLysPheLysGly 85
 RESULT 9
 Q6PP95 PRELIMINARY; PRT; 464 AA.
 AC Q6PP95;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2B6 II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2B6 II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057672; AAH57672.1; -;
 DR HSSP; P01865; IKB5.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG CL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;
 Alignment Scores:
 Pred. No.: 6.12 Length: 464
 Score: 72.70 Matches: 13
 Percent Similarity: 60.00% Conservative: 5
 Best Local Similarity: 43.33% Mismatches: 9
 Query Match: 49.12% Indels: 3
 DB: 2 Gaps: 0
 NOLAN463-2B.SEQ (1-84) x Q6PP95 (1-464)
 Qy 1 CGGGCGAGTCAGGTATTAGCAGCTGGTATGCCATCTCTCTCTGGTACTGTGATACC 60
 Db 59 ArgSerGlyGinglyLeu---GluTrpIleIleIleArgIleTyProGlyThrGlySerThr 77
 Qy 61 ACATACAGCCCGTCTCTCCCAAGGC 84
 Db 78 TyrTyraenGluLysPheLysGly 85
 RESULT 10
 Q99LC4 PRELIMINARY; PRT; 463 AA.
 ID Q99LC4
 AC Q99LC4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Igh-4 protein.
 GN Name=Igh-4;


```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
CC Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NPb antibodies.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00536; AAA38605.1; -.
DR PIR; A02031; HVMS3.
DR HSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003596; Igh_V.
DR Pfam; PF00047; Igh_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 3.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Alignment Scores:
Pred. No.: 21.5 Length: 117
Score: 67.70 Matches: 12
Percent Similarity: 58.62% Conservative: 5
Best Local Similarity: 41.38% Mismatches: 9
Query Match: 45.74% Indels: 3
DB: 1 Gaps: 0

NOLAN463-2B-SEQ (1-84) x HV05_MOUSE (1-117)
QY 1 CGGGCGAGTCAGGCTATTAGCAGCTGGTATGCCATCATCTATCTGTGCTGATACC 60
Db 59 ArgProGlyGlnGlyLeu---GluTrpIleGlyAsnIleTyProSerAspSerGluThr 77
QY 61 ACATACAGCCGCTCTCCAA 81
Db 78 HisTyAsnGlnLysPheLys 84

RESULT 13
QY1V67 PRELIMINARY; PRT; 143 AA.
AC QY1V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (fragment).
GN Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -.
DR EMBL; AB069914; BAB63930.1; -.
DR PIR; S26744; S26744.
DR HSP; P01751; IAGW.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44BEBF CRC64;

Alignment Scores:
Pred. No.: 29.8 Length: 143
Score: 66.70 Matches: 12
Percent Similarity: 56.67% Conservative: 5
Best Local Similarity: 40.00% Mismatches: 10
Query Match: 45.07% Indels: 3
DB: 2 Gaps: 0

NOLAN463-2B-SEQ (1-84) x QY1V67 (1-143)
QY 1 CGGGCGAGTCAGGCTATTAGCAGCTGGTATGCCATCATCTATCTGTGCTGATACC 60
Db 40 ArgProGlyGlnGlyLeu---GluTrpIleGlyValIleAspProSerAspSerTyThr 58
QY 61 ACATACAGCCGCTCTCCAAAGC 84
Db 59 AsnTyAsnGlnLysPheLysGly 66

RESULT 14
QY1V67 PRELIMINARY; PRT; 236 AA.
ID Q6GMX8
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
EX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:02:48 ; Search time 114 Seconds

(without alignments)
549.607 Million cell updates/sec

Title: DELETED1

Perfect score: 140

Sequence: 1 GAATCAATCATAGTGAAG.....ATATTAGACAGCTGTTAGCC 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120124_18790/app_query.fasta_1.263
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOFCIL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A @CGN 1.1 224 @runat_04082005_120124_18790 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

A_Geneseq 16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 113.1 | 80.8 | 249 | 5 | ABP45310 Human Bly |
| 2 | 113.1 | 80.8 | 249 | 7 | ADG96137 Single ch |
| 3 | 93.8 | 67.0 | 250 | 5 | ADP44982 Human Bly |
| 4 | 93.8 | 67.0 | 250 | 7 | ADG95809 Single ch |
| 5 | 93.8 | 67.0 | 253 | 5 | ABP44943 Human Bly |
| 6 | 93.8 | 67.0 | 253 | 7 | ADG95770 Single ch |
| 7 | 92.4 | 66.0 | 80 | 2 | AAW62794 Amino aci |
| 8 | 92.4 | 66.0 | 97 | 2 | AAV05694 Multiple |
| 9 | 92.4 | 66.0 | 97 | 5 | ABG78212 Human Fv |
| 10 | 92.4 | 66.0 | 97 | 5 | ABG91903 Human ant |

| | | | | | |
|----|------|------|-----|---|--------------------|
| 11 | 92.4 | 66.0 | 97 | 6 | ABO27107 |
| 12 | 92.4 | 66.0 | 97 | 7 | ADB75646 Human ger |
| 13 | 92.4 | 66.0 | 97 | 7 | ADD28104 Lymphoma |
| 14 | 92.4 | 66.0 | 97 | 7 | ADF10048 VEGF anti |
| 15 | 92.4 | 66.0 | 97 | 7 | ADF10150 Antibody |
| 16 | 92.4 | 66.0 | 97 | 7 | ADF09942 Antibody |
| 17 | 92.4 | 66.0 | 97 | 7 | ADJ80323 VH gene 1 |
| 18 | 92.4 | 66.0 | 114 | 3 | ABO1949 Anti-Id1 |
| 19 | 92.4 | 66.0 | 114 | 3 | ABO1950 Anti-Id1 |
| 20 | 92.4 | 66.0 | 114 | 3 | ABO1953 Anti-Id1 |
| 21 | 92.4 | 66.0 | 114 | 3 | ABO1959 High affi |
| 22 | 92.4 | 66.0 | 114 | 3 | ABO1952 Anti-Id1 |
| 23 | 92.4 | 66.0 | 114 | 3 | ABO1955 Streptativ |
| 24 | 92.4 | 66.0 | 114 | 3 | ABO1956 Streptativ |
| 25 | 92.4 | 66.0 | 114 | 3 | ABO1948 Wild-type |
| 26 | 92.4 | 66.0 | 114 | 7 | ADG70086 Diversifi |
| 27 | 92.4 | 66.0 | 114 | 7 | ADG70013 Diversifi |
| 28 | 92.4 | 66.0 | 115 | 2 | AAE66324 Human imm |
| 29 | 92.4 | 66.0 | 117 | 4 | AAW60904 Human bra |
| 30 | 92.4 | 66.0 | 117 | 4 | ABG55317 Human liv |
| 31 | 92.4 | 66.0 | 117 | 5 | ABG43454 Human pep |
| 32 | 92.4 | 66.0 | 118 | 6 | ADA89246 Human ant |
| 33 | 92.4 | 66.0 | 122 | 7 | ADK17418 Anti-huma |
| 34 | 92.4 | 66.0 | 122 | 8 | ADG42840 scFv Ab12 |
| 35 | 92.4 | 66.0 | 123 | 2 | AAW03757 Anti-rhes |
| 36 | 92.4 | 66.0 | 125 | 6 | ADA89266 Human ant |
| 37 | 92.4 | 66.0 | 125 | 6 | ADA89274 Human ant |
| 38 | 92.4 | 66.0 | 139 | 3 | AAV99556 Human LH1 |
| 39 | 92.4 | 66.0 | 139 | 6 | ABR42859 Tumour-ep |
| 40 | 92.4 | 66.0 | 139 | 7 | ABW02445 Human mon |
| 41 | 92.4 | 66.0 | 142 | 6 | ABP96287 Anti-hTNF |
| 42 | 92.4 | 66.0 | 154 | 6 | ABP96293 Human ant |
| 43 | 92.4 | 66.0 | 190 | 2 | AAV34304 IGM antib |
| 44 | 92.4 | 66.0 | 202 | 2 | AAV34303 IGM antib |
| 45 | 92.4 | 66.0 | 205 | 2 | AAV34299 IGM antib |

ALIGNMENTS

RESULT 1

ABP45310
ID ABP45310 standard; protein; 249 AA.

XX AC ABP45310;

XX AC

DT 19-AUG-2002 (first entry)

XX Human BlyS binding scFv SEQ ID 1321.

DE Human BlyS binding scFv SEQ ID 1321.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX OS

XX WO200202641-A1.

XX PD 10-JAN-2002.

XX PD

XX 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
 Qy 48 ----- 48
 Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
 Qy 48 ----- 48
 Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGlyGly 129
 Qy 48 ----- 48
 Db 130 GlySerGlyGlyGlySerGlyGlyGlyGlyGlySerAspIleValMetThrGlnSerPro 149
 Qy 49 -----CGGGCCGAGTCAGGAT 63
 Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
 Qy 64 ATTACGACGTGGTTAGCC 81
 Db 170 IleSerSerTrpLeuAla 175

RESULT 3

ABP44982

ID ABP44982 standard; protein; 250 AA.

XX AC ABP44982;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 993.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;

XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX FT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

XX FT diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 1586-1587; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to

XX CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the

XX CC tumour necrosis factor (TNF) super family and induces B cell

XX CC proliferation and differentiation. The antibodies of the invention have

XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

XX CC antirheumatic and antiAIDS activity and can be used in vaccines to

XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

SQ Sequence 250 AA;

Alignment Scores:

Pred. No.: 0.00327 Length: 250
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 5 Gaps: 1

DELETED1 (1-81) x ABP44982 (1-250)

Qy 1 GAATCATCATAGTCGAGCAGCACCACTACACCGCTCTCTCAGAGTCGGCGG----- 54

Db 50 GluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

Qy 55 AGTCAGGATATTAGCAGC 72

Db 70 SerGlnAspThrSerAsn 75

RESULT 4

ADG95809

ID ADG95809 standard; protein; 250 AA.

XX AC ADG95809;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 993.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

XX KW B cell proliferation; differentiation; scFv; myasthenia gravis;

XX KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

XX KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

XX KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 XX PT (Blys), useful for detecting and treating diseases or disorders e.g.
 XX PT rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 993; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind

XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

XX CC chromosome 13q34 and encodes a protein that is a member of the tumour

CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 250 AA;

Alignment Scores:
 Pred. No.: 0.00327 Length: 250
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 7 Gaps: 1

DELETED1 (1-81) x ADG95809 (1-250)

QY 1 GAATCATCATAGTGGAGCACCACCTACAAACCGTCTCTCAAGATCGGGCG----- 54
 Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69
 QY 55 AGTCAGGATATTAGCAGC 72
 Db 70 SerGlnAspThrSerAsn 75

RESULT 5

ID ABP44943
 ID ABP44943 standard; protein; 253 AA.
 AC ABP44943;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 954.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS

XX

XX WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

XX 16-JUN-2000; 2000US-0212210P.

PR

PR 17-OCT-2000; 2000US-0240816P.

PR

PR 16-MAR-2001; 2001US-0276248P.

PR

PR 21-MAR-2001; 2001US-0277379P.

PR

PR 25-MAY-2001; 2001US-0293499P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI; 2002-114799/15.
 XX
 DR Antibodies against B lymphocyte stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 PT
 PT Claim 1; Page 1540-1541; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys in
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 253 AA;

Alignment Scores:
 Pred. No.: 0.00328 Length: 253
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 5 Gaps: 1

DELETED1 (1-81) x ABP44943 (1-253)

QY 1 GAATCATCATAGTGGAGCACCACCTACAAACCGTCTCTCAAGATCGGGCG----- 54
 Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69

QY 55 AGTCAGGATATTAGCAGC 72

Db 70 SerGlnAspThrSerAsn 75

RESULT 6

ADG95770
 ID ADG95770 standard; protein; 253 AA.

XX ADG95770;

XX

DT 11-MAR-2004 (first entry)

XX

DE Single chain antibody that immunospecifically binds Blys SeqID 954.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

KW B cell proliferation; differentiation; scFv; myasthenia gravis;

KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS

XX WO2003055979-A2.

PN

XX 10-JUL-2003.

PD

XX 14-NOV-2002; 2002WO-US036496.

PF

XX 16-NOV-2001; 2001US-0331469P.

PR

PR 19-DEC-2001; 2001US-0340817P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 XX WPI; 2003-505530/47.
 XX
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 XX Example 1; SEQ ID NO 954; 394pp; English.
 XX
 XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antisthmatic, anti-allergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 253 AA;

Alignment Scores:
 Pred. No.: 0.00328 Length: 253
 Score: 93.80 Matches: 20
 Percent Similarity: 80.77% Conservative: 1
 Best Local Similarity: 76.92% Mismatches: 3
 Query Match: 67.00% Indels: 2
 DB: 7 Gaps: 1

DELETED1 (1-81) x ADG95770 (1-253)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCTCAAGAGTCGGGCG----- 54
 Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuAenSerArgValThrIle 69

Qy 55 AGTCAGGATATAGCAGC 72
 Db 70 SerGlnAspThrSerAsn 75

RESULT 7
 AAW62794
 ID AAW62794 standard; peptide; 80 AA.
 XX
 XX AAW62794;
 AC
 DT 23-SEP-1998 (first entry)
 XX
 XX Amino acid sequence of a human antibody fragment.
 DE
 XX Human; immunoglobulin; Ig; transgenic; non-human mammal;
 KW inactivated endogenous Ig locus; B-cell development;
 KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
 KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
 XX production; antibody.

OS Homo sapiens.
 XX WO9824893-A2.
 XX
 XX 11-JUN-1998.
 PD
 XX 03-DEC-1997; 97WO-US023091.
 PF
 XX 03-DEC-1996; 96US-00759620.
 PR
 XX (ABGE-) ABGENIX INC.
 PA
 XX Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
 PI WPI; 1998-333314/29.
 XX
 XX New transgenic non-human mammals - having an inactivated immunoglobulin
 DR locus and a near complete human immunoglobulin locus, used for production
 XX of human antibodies.
 PT
 XX Disclosure; Page 71; 128pp; English.
 PS
 XX AAW62793-822 represent fragments of human antibodies produced by
 CC transgenic Xenomice, created using the method of the invention. The
 CC specification describes a transgenic non-human mammal which has genome
 CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
 CC locus, so that the mammal does not display normal B-cell development. The
 CC modified genome also has an inserted human heavy chain Ig locus in
 CC germline configuration, the human heavy chain Ig locus comprising a human
 CC micro constant region and regulatory and switch sequences, human J-H
 CC genes, human D-H genes, and human V-H genes and an inserted human kappa
 CC light chain Ig locus in germline configuration, the human kappa light
 CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
 CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
 CC selected to restore normal B-cell development in the mammal. The
 CC transgenic animals have a near complete human Ig locus, including both a
 CC human heavy chain locus and a human kappa light chain locus. They can be
 CC used for the production of human antibodies when exposed to particular
 CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
 CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
 XX
 SQ Sequence 80 AA;

Alignment Scores:
 Pred. No.: 0.00354 Length: 80
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 2 Gaps: 0

DELETED1 (1-81) x AAW62794 (1-80)

Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCTCAAGAGTCGGGCGAGTCAG 60
 Db 33 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuAenSerArgValThr--- 51

Qy 61 GATATTAGC 69
 Db 52 ---Ileser 53

RESULT 8
 AAY05694
 ID AAY05694 standard; protein; 97 AA.
 XX
 XX AAY05694;
 AC
 XX 19-JUL-1999 (first entry)
 DT
 XX Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
 DE
 XX Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
 KW heavy chain variable region; VH gene; somatic hypermutation;
 KW

B-cell clonality; RA gene; diagnosis; human.

Homo sapiens.

Key Location/Qualifiers

Region 1..30

/label= FR1

Misc-difference 8

/note= "encoded by GGC"

Misc-difference 13

/note= "replaces Glu of RA"

Misc-difference 14

/note= "encoded by CCT"

Misc-difference 23

/note= "replaces Gly of RA"

Misc-difference 25

/note= "replaces Phe of RA"

Misc-difference 30

/note= "replaces Gly of RA"

Region 31..36

/label= CDR1

Misc-difference 31

/note= "replaces Gly of RA"

Misc-difference 32

/note= "replaces Phe of RA"

Region 37..50

/label= FR2

Region 51..66

/label= CDR2

Misc-difference 56

/note= "replaces Asn of RA"

Misc-difference 57

/note= "replaces Ser of RA"

Misc-difference 58

/note= "replaces Lys of RA"

Region 67..97

/label= FR3

Misc-difference 71

/note= "replaces Leu of RA"

Misc-difference 81

/note= "replaces Arg of RA"

WO9915696-A1.

01-APR-1999.

17-SEP-1998; 98WO-CA000873.

19-SEP-1997; 97CA-02216595.

04-NOV-1997; 97CA-02220245.

(QINY/) QIN Y.

Qin Y;

WPI; 1999-276985/23.

N-PSDB; AAX25318.

Determination of B-cell clonality by amplification or enzymatic

digestion.

Disclosure; Fig 9D; 67pp; English.

This sequence represents a heavy chain variable region (VH) as predicted

from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal

fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF

B-cells were obtained from 4 MS patients (see AAX25316-19). Differences

in nucleotide and predicted amino acid (see AAY05691-94) sequences were

compared with the closest known germline VH genes; for 4d76, this was RA.

The results provided direct evidence that intrathecal clonally expanded B

-cells from the CSF of MS patients are hypermutated postgerminal centre

antibody-forming or memory lymphocytes that have undergone antigen

selection. This finding implicates an important pathogenic pathway for

the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy

SQ Sequence 97 AA;

Alignment Scores:

Pred. No.: 0.00375 Length: 97

Score: 92.40 Matches: 19

Percent Similarity: 74.07% Conservative: 1

Best Local Similarity: 70.37% Mismatches: 1

Query Match: 66.00% Indels: 6

DB: 2 Gaps: 0

DELETED1 (1-81) x AAY05694 (1-97)

QY 1 GAATCAATCATAGTGAAGCAACCACTACAAACCGTCTCTCAAGAGTCCGGCGAGTCAG 60

Db 50 GlulleAsnHisserGlySerThrAsnTrAsnProSerLeuLysSerArgValThr--- 68

QY 61 GATATTAGC 69

Db 69 ---ileSer 70

RESULT 9

ABG78212

ID ABG78212 standard; protein; 97 AA.

AC ABG78212;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #87.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KW lymphoma; myeloma; blastoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

WO200259264-A2.

01-AUG-2002.

31-DEC-2001; 2001WO-US049440.

29-DEC-2000; 2000US-00751181.

(BIOT-) BIO-TECHNOLOGY GEN CORP.

Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

Plaksin D, Peretz T;

WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

or fragment, or construct of fragment with enhanced binding

characteristics so as to selectively bind target cell in favor of other

cells.

Claim 13; Page 193; 232pp; English.

The invention relates to a peptide or polypeptide comprising an Fv

molecule, a construct or fragments or a construct of a fragment with

enhanced binding characteristics which selectively and/or specifically

binds to a target cell in favour of other cells, where binding is

primarily determined by a first hypervariable region and Fv is a single

chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

association with or attached, coupled, combined, linked or fused to a

pharmaceutical agent, is useful in the manufacture of a medicament, where

xx CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one

XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies

XX Sequence 97 AA;
 SQ

Alignment Scores:
 Pred. No.: 0.00375 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 6 Gaps: 0

DELETED1 (1-81) x ABO27107 (1-97)

Qy 1 GAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
 |||||
 Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
 |||||

Qy 61 GATATTAGC 69
 |||||
 Db 69 ---IleSer 70

RESULT 12
 ADB75646
 ID ADB75646 standard; protein; 97 AA.
 XX
 AC ADB75646;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human protein relating to the invention SEQ ID NO:55.
 XX
 KW antibody library; CD1 region; CD2 region; VH region; VL region;
 KW immunoglobulin; CD3 region; TW1 scFv; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003044198-A1.
 XX
 PD 30-MAY-2003.
 XX
 PF 22-NOV-2002; 2002WO-JP012236.
 XX
 PR 22-NOV-2001; 2001JP-00358602.
 XX
 PA (UYKE-) UNIV KEIO.
 XX
 PI Shimizu N, Takayanagi A, Okui M;
 XX
 DR WPI; 2003-449818/42.
 XX
 PT Highly stable artificial antibody libraries with super-repository and

PT little contamination from unexpressible ones, useful as tool in
 PT proteomics and e.g. for diagnosis and treating various diseases.
 XX
 PS Disclosure; Page 101; 108pp; Japanese.
 XX
 CC The invention relates to a novel artificial single-stranded antibody
 CC library with superior-repository. The library is created by using a cDNA
 CC library as template for amplifying a fragment containing the CD1 and CD2
 CC regions of the VH or VL region of immunoglobulin gene and a fragment
 CC containing the CD3 region by PCR, respectively, producing VH and VL
 CC libraries, transferring into a host, and displaying the single-stranded
 CC antibody on a phage surface. An antibody library of the invention is
 CC useful as a tool in proteomics and antibody chips and filters, for
 CC screening ligands for antigens, and for studying protein-DNA interaction,
 CC diagnosis and treating various diseases. The present sequence represents
 CC a protein of the invention.

XX Sequence 97 AA;
 SQ

Alignment Scores:
 Pred. No.: 0.00375 Length: 97
 Score: 92.40 Matches: 19
 Percent Similarity: 74.07% Conservative: 1
 Best Local Similarity: 70.37% Mismatches: 1
 Query Match: 66.00% Indels: 6
 DB: 7 Gaps: 0

DELETED1 (1-81) x ADB75646 (1-97)

Qy 1 GAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
 |||||
 Db 50 GlulleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
 |||||

Qy 61 GATATTAGC 69
 |||||
 Db 69 ---IleSer 70

RESULT 13
 ADD28104
 ID ADD28104 standard; protein; 97 AA.
 XX
 AC ADD28104;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Lymphoma related immunoglobulin variable region F5.
 XX
 KW B-cell; malignant; immunoglobulin; immunoglobulin variable region;
 KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
 KW cytostatic; gene therapy; glycosylation inhibitor;
 KW non-Hodgkin's lymphoma.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO2003074059-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 24-FEB-2003; 2003WO-GB000783.
 XX
 PR 07-MAR-2002; 2002GB-00005395.
 XX
 PA (CANC-) CANCER RES TECHNOLOGY LTD.
 XX
 PI Zhu D, Stevenson F;
 XX
 DR WPI; 2003-902720/82.
 XX
 CC Classifying a B-cell as malignant or normal by isolating a sequence
 PT representing an Ig variable region from the B cell, detecting the
 PT presence of a glycosylation site and classifying the cell as malignant or
 PT normal.

XX Disclosure; Fig 4; 61pp; English.

XX The present invention describes a method for classifying a B-cell as

CC malignant or normal comprising: (a) isolating a sequence representing an

CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the

CC presence of a glycosylation site; and (c) classifying the cell as

CC malignant or normal on the basis of the presence or absence of a

CC glycosylation site. Also described: (1) treating a patient suffering from

CC or at risk of having lymphoma; (2) screening for substances capable of

CC inhibiting glycosylation of the Ig variable region of the B cell receptor

CC ; and (3) screening for substances (S) capable of inhibiting the

CC interaction between lectins of the type found in the germinal centre and

CC N-glycans found on the surface of Ig of lymphoma cells. (S) has

CC cystostatic activity, and can be used in gene therapy, and as a

CC glycosylation inhibitor. The method is useful in classifying a B-cell as

CC malignant or normal. The glycosylation inhibitor is useful in preparing a

CC medicament for treating non-Hodgkin's lymphoma. The present sequence

CC represents an Ig variable region sequence which is used in the

CC exemplification of the present invention.

SQ Sequence 97 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00375 | Length: | 97 |
| Score: | 92.40 | Matches: | 19 |
| Percent Similarity: | 74.07% | Conservative: | 1 |
| Best Local Similarity: | 70.37% | Mismatches: | 1 |
| Query Match: | 66.00% | Indels: | 6 |
| DB: | 7 | Gaps: | 0 |

DELETED1 (1-81) x ADD28104 (1-97)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACACCCGCTCTCTCAAGAGTGGCGAGTCAG 60
 Db 50 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 68
 Qy 61 GATATTAGC 69
 Db 69 ---IleSer 70

RESULT 14

ID ADF10048 standard; protein; 97 AA.

AC ADF10048;

DT 12-FEB-2004 (first entry)

DE VEGF antibody heavy chain variable region VH_4-34.

XX Antibody; stability; solubility; antigen binding affinity;

KW variable region; human; VEGF.

XX Homo sapiens.

OS WO2003074679-A2.

PN 12-SEP-2003.

PD 03-MAR-2003; 2003WO-US006598.

PF 01-MAR-2002; 2002US-0360843P.

PR 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies

PT comprises analyzing the interactions of amino acids at variable

PT positions.

XX Example 6; Fig 16a; 135pp; English.

XX The present invention relates to a method for optimizing at least one

CC physico-chemical property of an antibody by a computational screening

CC method. The method comprises: receiving a template antibody structure;

CC selecting at least one variable position belonging to the antibody

CC structure; selecting at least one amino acid to be considered at the

CC variable position(s); analyzing the interaction of each selected amino

CC acid at each variable position with at least part of the remainder of the

CC antibody, including the selected amino acids at other variable positions;

CC and identifying a set of at least one antibody sequence with at least one

CC optimized physico-chemical property. The method is useful for optimizing

CC the physico-chemical properties of an antibody, especially the stability,

CC solubility, or antigen binding affinity. The optimized antibody may be

CC useful for treating a patient. The present sequence is an antibody

CC variable region sequence used to illustrate the invention.

SQ Sequence 97 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00375 | Length: | 97 |
| Score: | 92.40 | Matches: | 19 |
| Percent Similarity: | 74.07% | Conservative: | 1 |
| Best Local Similarity: | 70.37% | Mismatches: | 1 |
| Query Match: | 66.00% | Indels: | 6 |
| DB: | 7 | Gaps: | 0 |

DELETED1 (1-81) x ADF10048 (1-97)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACACCCGCTCTCTCAAGAGTGGCGAGTCAG 60
 Db 50 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 68
 Qy 61 GATATTAGC 69
 Db 69 ---IleSer 70

RESULT 15

ID ADF10150 standard; protein; 97 AA.

AC ADF10150;

DT 12-FEB-2004 (first entry)

DE Antibody heavy chain variable region VH_4-34.

XX Antibody; stability; solubility; antigen binding affinity;

KW variable region; human.

XX Homo sapiens.

OS WO2003074679-A2.

PN 12-SEP-2003.

PD 03-MAR-2003; 2003WO-US006598.

PF 01-MAR-2002; 2002US-0360843P.

PR 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies

PT comprises analyzing the interactions of amino acids at variable

XX positions.

PS Example 16; Fig 40a; 135pp; English.

XX

CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.

XX

SQ Sequence 97 AA;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 0.00375 | Length: | 97 |
| Score: | 92.40 | Matches: | 19 |
| Percent Similarity: | 74.07% | Conservative: | 1 |
| Best Local Similarity: | 70.37% | Mismatches: | 1 |
| Query Match: | 66.00% | Indels: | 6 |
| DB: | 7 | Gaps: | 0 |

DELETED1 (1-81) x ADF10150 (1-97)

| | | | |
|----|----|---|-----|
| Qy | 1 | GAATTCATCATAGTGGAGCACCACCACTACCAACCGTCTCTCAAGAGTCGGCGAGTCAG | 60 |
| Db | 50 | | ::: |
| Qy | 61 | GATATTAGC | 69 |
| Db | 69 | ---IleSer | 70 |

Search completed: August 4, 2005, 19:34:16
Job time : 120 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:25:09 ; Search time 30 Seconds
(without alignments)
403.105 Million cell updates/sec

Title: DELETED1

Perfect score: 140

Sequence: 1 GAATCAATCATAGTGGAG.....ATATTAGCAGCTGTTAGCC 81

Scoring table:

| | | |
|----------|-------------|-------------|
| BLOSUM62 | Xgapop 10.0 | Xgapext 0.1 |
| | Ygapop 10.0 | Ygapext 0.1 |
| | Fgapop 6.0 | Fgapext 0.1 |
| | Delop 6.0 | Delext 0.1 |

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120126_18820/app_query.fasta_1.263
-DB=Issued Patents AA -QWMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN463-3A @CGN 1.1 46 @runat_04082005_120126_18820 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1
```

Database : Issued Patents AA:*

| | |
|----|--|
| 1: | /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* |
| 2: | /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* |
| 3: | /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* |
| 4: | /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* |
| 5: | /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:* |
| 6: | /cgn2_6/ptodata/1/iaa/backfiles1.pep:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 92.4 | 66.0 | 116 | 3 | US-08-545-809A-118 |
| 2 | 92.4 | 66.0 | 123 | 3 | US-08-793-450-4 |
| 3 | 92.4 | 66.0 | 139 | 4 | US-09-203-768A-2 |
| 4 | 92.4 | 66.0 | 472 | 3 | US-08-793-450-8 |
| 5 | 87.4 | 62.4 | 429 | 4 | US-09-372-425A-6 |
| 6 | 84.4 | 60.3 | 118 | 3 | US-09-025-769B-25 |
| 7 | 84.4 | 60.3 | 118 | 4 | US-09-490-070A-25 |
| 8 | 84.4 | 60.3 | 118 | 4 | US-09-490-153-25 |
| 9 | 84.4 | 60.3 | 118 | 4 | US-09-490-324-25 |
| 10 | 81 | 57.9 | 120 | 3 | US-08-545-809A-137 |
| 11 | 80.7 | 57.6 | 130 | 3 | US-08-466-151-5 |
| 12 | 80.7 | 57.6 | 130 | 3 | US-08-466-163B-5 |

| | | | | | | |
|----|------|------|-----|---|--------------------|-------------------|
| 13 | 80.7 | 57.6 | 130 | 4 | US-09-802-096-5 | Sequence 5, Appli |
| 14 | 80.7 | 57.6 | 130 | 4 | US-09-802-077-5 | Sequence 5, Appli |
| 15 | 79.4 | 56.7 | 147 | 4 | US-09-471-276-835 | Sequence 835, App |
| 16 | 79.4 | 56.7 | 447 | 4 | US-09-372-425A-2 | Sequence 2, Appli |
| 17 | 77 | 55.0 | 119 | 2 | US-08-428-197-16 | Sequence 16, Appl |
| 18 | 77 | 55.0 | 119 | 5 | PCT-US93-10555-16 | Sequence 16, Appl |
| 19 | 76.4 | 54.6 | 112 | 3 | US-09-344-587-14 | Sequence 14, Appl |
| 20 | 75.9 | 54.6 | 118 | 2 | US-08-652-816A-13 | Sequence 13, Appl |
| 21 | 74.4 | 53.1 | 120 | 4 | US-09-424-840B-20 | Sequence 20, Appl |
| 22 | 73.4 | 52.4 | 21 | 3 | US-08-918-148-45 | Sequence 45, Appl |
| 23 | 73.4 | 52.4 | 21 | 4 | US-09-138-091A-45 | Sequence 45, Appl |
| 24 | 73.4 | 52.4 | 76 | 3 | US-08-851-362D-22 | Sequence 22, Appl |
| 25 | 73.4 | 52.4 | 96 | 3 | US-08-851-362D-35 | Sequence 35, Appl |
| 26 | 73.4 | 52.4 | 116 | 3 | US-08-545-809A-140 | Sequence 140, App |
| 27 | 73.4 | 52.4 | 117 | 3 | US-08-851-362D-48 | Sequence 48, Appl |
| 28 | 73.4 | 52.4 | 118 | 3 | US-08-545-809A-142 | Sequence 142, App |
| 29 | 73.4 | 52.4 | 119 | 3 | US-09-025-769B-39 | Sequence 39, Appl |
| 30 | 73.4 | 52.4 | 119 | 3 | US-09-025-769B-65 | Sequence 65, Appl |
| 31 | 73.4 | 52.4 | 119 | 4 | US-09-490-070A-39 | Sequence 39, Appl |
| 32 | 73.4 | 52.4 | 119 | 4 | US-09-490-070A-65 | Sequence 65, Appl |
| 33 | 73.4 | 52.4 | 119 | 4 | US-09-490-153-39 | Sequence 39, Appl |
| 34 | 73.4 | 52.4 | 119 | 4 | US-09-490-153-65 | Sequence 65, Appl |
| 35 | 73.4 | 52.4 | 119 | 4 | US-09-490-324-39 | Sequence 39, Appl |
| 36 | 73.4 | 52.4 | 119 | 4 | US-09-490-324-65 | Sequence 65, Appl |
| 37 | 73.4 | 52.4 | 139 | 4 | US-09-471-276-837 | Sequence 837, App |
| 38 | 73.4 | 52.4 | 244 | 3 | US-08-918-148-79 | Sequence 79, Appl |
| 39 | 73.4 | 52.4 | 244 | 4 | US-09-138-091A-77 | Sequence 77, Appl |
| 40 | 73 | 52.1 | 100 | 4 | US-09-726-219A-169 | Sequence 169, App |
| 41 | 72.4 | 51.7 | 140 | 4 | US-09-471-276-850 | Sequence 850, App |
| 42 | 72.4 | 51.7 | 240 | 2 | US-07-956-399-2 | Sequence 2, Appli |
| 43 | 72 | 51.4 | 95 | 4 | US-09-471-276-882 | Sequence 882, App |
| 44 | 72 | 51.4 | 116 | 3 | US-08-545-809A-92 | Sequence 92, Appl |
| 45 | 72 | 51.4 | 119 | 3 | US-08-767-128-18 | Sequence 18, Appl |

ALIGNMENTS

RESULT 1

```
US-08-545-809A-118
; Sequence 118, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
```

```
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:
Pred. No.: 0.000397 Length: 116
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 3 Gaps: 0

DELETED1 (1-81) x US-08-545-809A-118 (1-116)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 69 GlulleasnHisSerGlySerThrAsnTyraSnProSerLeuLySerArgValThr---- 87

Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 2
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITE, CRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-4
```

```
Alignment Scores:
Pred. No.: 0.000405 Length: 123
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 3 Gaps: 0

DELETED1 (1-81) x US-08-793-450-4 (1-123)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleasnHisSerGlySerThrAsnTyraSnProSerLeuLySerArgValThr---- 68

Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 3
US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:
Pred. No.: 0.000423 Length: 139
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 4 Gaps: 0

DELETED1 (1-81) x US-09-203-768A-2 (1-139)

Qy 1 GAAATCAATCATAGTGGGAAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 69 GlulleasnHisSerGlySerThrAsnTyraSnProSerLeuLySerArgValThr---- 87

Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITE, CRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
```



```
;
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-25

Alignment Scores:
Pred. No.: 0.0049 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 3 Gaps: 0

DELETED1 (1-81) x US-09-025-769B-25 (1-118)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6596248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.: 0.0049 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

DELETED1 (1-81) x US-09-490-070A-25 (1-118)
Qy 1 GAAATCAATCATAGTGAAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68

Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25
```


Alignment Scores:
Pred. No.: 0.0049 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

DELETED1 (1-81) x US-09-490-153-25 (1-118)

QY 1 GAATCAATCATAGTGGAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleTyHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68

QY 61 GATATTAGC 69
|||||
Db 69 ---lleSer 70

RESULT 9

US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-490-324-25

Alignment Scores:
Pred. No.: 0.0049 Length: 118
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2

Query Match: 60.29% Indels: 6
DB: 4 Gaps: 0

DELETED1 (1-81) x US-09-490-324-25 (1-118)

QY 1 GAATCAATCATAGTGGAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleTyHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68

QY 61 GATATTAGC 69
|||||
Db 69 ---lleSer 70

RESULT 10

US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-137

Alignment Scores:
Pred. No.: 0.0143 Length: 120
Score: 81.00 Matches: 15
Percent Similarity: 79.17% Conservative: 4
Best Local Similarity: 62.50% Mismatches: 5
Query Match: 57.86% Indels: 0
DB: 3 Gaps: 0

DELETED1 (1-81) x US-08-545-809A-137 (1-120)

QY 1 GAATCAATCATAGTGGAGCACCACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 69 GlulleHisSerGlySerThrTyAsnProSerLeuLysSerArgIleThrMet 88

QY 61 GATATTAGC 72
|||

Db 89 SerValAspThr 92

RESULT 11

US-08-466-151-5

; Sequence 5, Application US/08466151

; Patent No. 6037453

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,151

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466163

; FILING DATE: 06-Jun-1995

; APPLICATION NUMBER: 08/405617

; FILING DATE: 15-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/185899

; FILING DATE: 26-JAN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/879495

; FILING DATE: 07-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/744768

; FILING DATE: 14-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P0718P2C1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-466-151-5

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 0.0162 | Length: | 130 |
| Score: | 80.70 | Matches: | 18 |
| Percent Similarity: | 47.92% | Conservative: | 5 |
| Best Local Similarity: | 37.50% | Mismatches: | 2 |
| Query Match: | 57.64% | Indels: | 23 |
| DB: | 3 | Gaps: | 2 |

DELETED1 (1-81) x US-08-466-151-5 (1-130)

Qy 4 ATCAATCATAGTGGAGACCAACTACACCGTCTCTCAAGAGTCGGCGAGT----- 57

Db 52 IleAsnHisSerGlyThrSerTyAsnProSerLeuLysSerArgIleSerIleThr 71

Qy 58 CAGGATATTAGC----- 69

Db 72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy 70 -----AGCTGGTTA 78

Db 92 AlaThrTyTyrcysAlaTrpVal 99

RESULT 12

US-08-466-163B-5

; Sequence 5, Application US/08466163B

; Patent No. 6329509

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Immunoglobulin Variants

; FILE REFERENCE: P0718P2C1D1

; CURRENT APPLICATION NUMBER: US/08/466,163B

; CURRENT FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 5

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Mus musculus

US-08-466-163B-5

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 0.0162 | Length: | 130 |
| Score: | 80.70 | Matches: | 18 |
| Percent Similarity: | 47.92% | Conservative: | 5 |
| Best Local Similarity: | 37.50% | Mismatches: | 2 |
| Query Match: | 57.64% | Indels: | 23 |
| DB: | 3 | Gaps: | 2 |

DELETED1 (1-81) x US-08-466-163B-5 (1-130)

Qy 4 ATCAATCATAGTGGAGACCAACTACACCGTCTCTCAAGAGTCGGCGAGT----- 57

Db 52 IleAsnHisSerGlyThrSerTyAsnProSerLeuLysSerArgIleSerIleThr 71

Qy 58 CAGGATATTAGC----- 69

Db 72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAsnSerValThrThrGluAspThr 91

Qy 70 -----AGCTGGTTA 78

Db 92 AlaThrTyTyrcysAlaTrpVal 99

RESULT 13

US-09-802-096-5

; Sequence 5, Application US/09802096

; Patent No. 6685939

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

; FILE REFERENCE: P0718P2C3US

; CURRENT APPLICATION NUMBER: US/09/802,096

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

```
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:
Pred. No.: 0.0162 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 23
DB: 4 Gaps: 2

DELETED1 (1-81) x US-09-802-096-5 (1-130)
QY 4 ATCAATCATAGTGGAGACCACTACACCGGTCTCTCAAGAGTCGGCGAGT----- 57
Db 52 IleAsnHisSerGlyThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71
QY 58 CAGGATATTAGC----- 69
Db 72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAenSerValThrThrGluAspThr 91
QY 70 -----AGCTGGTTA 78
Db 92 AlaThrTyrCysAlaTrpVal 99

RESULT 14
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.: 0.0162 Length: 130
Score: 80.70 Matches: 18
Percent Similarity: 47.92% Conservative: 5
Best Local Similarity: 37.50% Mismatches: 23
Query Match: 57.64% Indels: 23
DB: 4 Gaps: 2

DELETED1 (1-81) x US-09-802-077-5 (1-130)
QY 4 ATCAATCATAGTGGAGACCACTACACCGGTCTCTCAAGAGTCGGCGAGT----- 57
Db 52 IleAsnHisSerGlyThrSerTyrAsnProSerLeuLysSerArgIleSerIleThr 71
QY 58 CAGGATATTAGC----- 69
Db 72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAenSerValThrThrGluAspThr 91
QY 70 -----AGCTGGTTA 78
Db 92 AlaThrTyrCysAlaTrpVal 99
```

```
Db 72 ArgAspThrSerLysAsnGlnPhePheLeuGlnLeuAenSerValThrThrGluAspThr 91
QY 70 -----AGCTGGTTA 78
Db 92 AlaThrTyrCysAlaTrpVal 99

RESULT 15
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET. 025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26...-1
US-09-471-276-835

Alignment Scores:
Pred. No.: 0.0254 Length: 147
Score: 79.40 Matches: 16
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 59.26% Mismatches: 3
Query Match: 56.71% Indels: 6
DB: 4 Gaps: 0

DELETED1 (1-81) x US-09-471-276-835 (1-147)
QY 1 GAATCATCATAGTGGAGACCACTACACCGGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 77 GluIleAspHisGlyGlyAsnThrAsnTyrAsnProSerLeuLysSerArgVal**** 95
QY 61 GATATTAGC 69
Db 96 ---IleSer 97

Search completed: August 4, 2005, 19:39:59
Job time : 32 secs
```

THIS PAGE BLANK (USE)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model
Run on: August 4, 2005, 19:38:05 ; Search time 105 Seconds
(without alignments)
602.328 Million cell updates/sec

Title: DELETED1

Perfect score: 140

Sequence: 1 GAAATCAATCACTAGTGAAG.....ATATTAGCAGCTGTTAGCC 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3A/runat_04082005_120128_18886/app_query.fasta_1.263
-DB=Published_Applications_AA -GPM=fastan -SUFFIX=rappb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=NOLAN463-3A@cgn 1 1 199 @runat_04082005_120128_18886
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1
-FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 113.1 | 80.8 | 249 | 10 | US-09-880-748-1321 |
| 2 | 113.1 | 80.8 | 249 | 15 | US-10-293-418-1321 |
| 3 | 96.4 | 68.9 | 115 | 17 | US-10-898-408-12 |
| 4 | 93.8 | 67.0 | 250 | 10 | US-09-880-748-993 |
| 5 | 93.8 | 67.0 | 250 | 15 | US-10-293-418-993 |
| 6 | 93.8 | 67.0 | 253 | 10 | US-09-880-748-954 |
| 7 | 93.8 | 67.0 | 253 | 15 | US-10-293-418-954 |
| 8 | 92.4 | 66.0 | 80 | 14 | US-10-078-958-2 |
| 9 | 92.4 | 66.0 | 97 | 14 | US-10-194-975-40 |
| 10 | 92.4 | 66.0 | 97 | 15 | US-10-308-817-83 |
| 11 | 92.4 | 66.0 | 97 | 15 | US-10-032-037B-87 |
| 12 | 92.4 | 66.0 | 97 | 15 | US-10-029-988B-87 |
| 13 | 92.4 | 66.0 | 97 | 15 | US-10-032-423A-87 |
| 14 | 92.4 | 66.0 | 97 | 15 | US-10-453-698-83 |
| 15 | 92.4 | 66.0 | 97 | 15 | US-10-029-926B-87 |
| 16 | 92.4 | 66.0 | 97 | 16 | US-10-379-392-47 |
| 17 | 92.4 | 66.0 | 114 | 17 | US-10-733-532-128 |
| 18 | 92.4 | 66.0 | 117 | 9 | US-09-864-761-44315 |
| 19 | 92.4 | 66.0 | 118 | 15 | US-10-371-942-90 |
| 20 | 92.4 | 66.0 | 118 | 17 | US-10-893-576-192 |
| 21 | 92.4 | 66.0 | 122 | 15 | US-10-360-828-63 |
| 22 | 92.4 | 66.0 | 125 | 15 | US-10-371-942-110 |
| 23 | 92.4 | 66.0 | 125 | 15 | US-10-371-942-118 |
| 24 | 92.4 | 66.0 | 139 | 14 | US-10-300-675-2 |
| 25 | 92.4 | 66.0 | 139 | 17 | US-10-910-124-2 |
| 26 | 92.4 | 66.0 | 139 | 17 | US-10-893-576-43 |
| 27 | 92.4 | 66.0 | 142 | 17 | US-10-484-790A-10 |
| 28 | 92.4 | 66.0 | 223 | 10 | US-09-972-656-66 |
| 29 | 92.4 | 66.0 | 229 | 10 | US-09-972-656-82 |
| 30 | 92.4 | 66.0 | 230 | 10 | US-09-972-656-72 |
| 31 | 92.4 | 66.0 | 249 | 10 | US-09-880-748-957 |
| 32 | 92.4 | 66.0 | 249 | 15 | US-10-293-418-957 |
| 33 | 92.4 | 66.0 | 250 | 10 | US-09-880-748-1413 |
| 34 | 92.4 | 66.0 | 250 | 15 | US-10-293-418-1413 |
| 35 | 92.4 | 66.0 | 253 | 10 | US-09-880-748-1333 |
| 36 | 92.4 | 66.0 | 253 | 15 | US-10-293-418-1333 |
| 37 | 92.4 | 66.0 | 254 | 10 | US-09-880-748-1659 |
| 38 | 92.4 | 66.0 | 254 | 15 | US-10-293-418-1659 |
| 39 | 92.4 | 66.0 | 450 | 17 | US-10-484-790A-17 |
| 40 | 92.4 | 66.0 | 453 | 17 | US-10-484-790A-18 |
| 41 | 90.4 | 64.6 | 246 | 10 | US-09-880-748-1847 |
| 42 | 90.4 | 64.6 | 246 | 15 | US-10-293-418-1847 |
| 43 | 90.3 | 64.5 | 123 | 14 | US-10-269-805-31 |
| 44 | 90.3 | 64.5 | 123 | 14 | US-10-269-805-55 |
| 45 | 88.4 | 63.1 | 255 | 10 | US-09-880-748-1642 |

ALIGNMENTS

RESULT 1
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

```
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.:      2.81e-05      Length:      249
Score:          113.10      Matches:      26
Percent Similarity: 20.63%      Conservative: 0
Best Local Similarity: 20.63%      Mismatches: 1
Query Match:      80.79%      Indels:      99
DB:              15          Gaps:      1

DELETED1 (1-81) x US-09-880-748-1321 (1-249)
Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCTCTCAAGAGT----- 48
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
Qy 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
Qy 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
Qy 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGly 129
Qy 48 ----- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149
Qy 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
Qy 64 ATTAGCAGCTGGTTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 2
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321

Alignment Scores:
Pred. No.:      2.81e-05      Length:      249
Score:          113.10      Matches:      26
Percent Similarity: 20.63%      Conservative: 0
Best Local Similarity: 20.63%      Mismatches: 1
Query Match:      80.79%      Indels:      99
DB:              15          Gaps:      1

DELETED1 (1-81) x US-10-293-418-1321 (1-249)
Qy 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGTCTCTCAAGAGT----- 48
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle 69
Qy 48 ----- 48
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAlaAlaAsp 89
Qy 48 ----- 48
Db 90 ThrAlaValTyrTyrCysAlaArgGlyProArgTyrTyrAspIleLeuThrGlyTyrArg 109
Qy 48 ----- 48
Db 110 TyrAsnTrpPheAspProTrpGlyArgGlyThrLeuValThrValSerSerGlyGly 129
Qy 48 ----- 48
Db 130 GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGlnSerPro 149
Qy 49 -----CGGGCGAGTCAGGAT 63
Db 150 SerThrLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 169
Qy 64 ATTAGCAGCTGGTTAGCC 81
Db 170 IleSerSerTrpLeuAla 175

RESULT 3
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12

Alignment Scores:
Pred. No.:      0.00314      Length:      115
Score:          96.40      Matches:      19
Percent Similarity: 41.18%      Conservative: 2
Best Local Similarity: 37.25%      Mismatches: 4
Query Match:      68.86%      Indels:      26
DB:              17          Gaps:      1
```

```

DELETED1 (1-81) x US-10-898-408-12 (1-115)

Qy 1 GAAATCAATCATAGTGGAGCACCACCTCTCTCAAGAGTCGGCGAGTCAG 60
    |||||
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69
    |||||
Qy 61 GATATTAGC----- 69
    |||||
Db 70 SerValAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAsp 89
    |||||
Qy 70 -----AGCTGG 75
    |||||
Db 90 ThrAlaValTyrTyrCysAlaArgValSerTrp 100
    |||||

RESULT 4
US-09-880-748-993
; Sequence 993, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-993

Alignment Scores:
Pred. No.: 0.00772 Length: 250
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 10 Gaps: 1

DELETED1 (1-81) x US-09-880-748-993 (1-250)

Qy 1 GAAATCAATCATAGTGGAGCACCACCTCTCTCAAGAGTCGGCGAGTCAG 54
    |||||
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69
    |||||
Qy 55 AGTCAGGATATTAGCAGC 72
    |||||
Db 70 SerGlnAspThrSerAsn 75
    |||||

RESULT 6
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954

Alignment Scores:
Pred. No.: 0.00774 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 10 Gaps: 1

DELETED1 (1-81) x US-10-898-408-12 (1-115)

Qy 1 GAAATCAATCATAGTGGAGCACCACCTCTCTCAAGAGTCGGCGAGTCAG 60
    |||||
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69
    |||||
Qy 55 AGTCAGGATATTAGCAGC 72
    |||||
Db 70 SerGlnAspThrSerAsn 75
    |||||

RESULT 5
US-10-293-418-993
; Sequence 993, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

```

```

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 993
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-993

Alignment Scores:
Pred. No.: 0.00772 Length: 250
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 10 Gaps: 1

DELETED1 (1-81) x US-10-293-418-993 (1-250)

Qy 1 GAAATCAATCATAGTGGAGCACCACCTCTCTCAAGAGTCGGCGAGTCAG 54
    |||||
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrMet 69
    |||||
Qy 55 AGTCAGGATATTAGCAGC 72
    |||||
Db 70 SerGlnAspThrSerAsn 75
    |||||

RESULT 6
US-09-880-748-954
; Sequence 954, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-954

Alignment Scores:
Pred. No.: 0.00774 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 10 Gaps: 1

```

```
DELETED1 (1-81) x US-09-880-748-954 (1-253)
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2
Alignment Scores:
Pred. No.: 0.0094 Length: 80
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 14 Gaps: 0
DELETED1 (1-81) x US-10-078-958-2 (1-80)
Qy 1 GAATCAATCATAGTGGAGCACCACCACTACAACCCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
Db 33 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 51
Qy 61 GATATTAGC 69
Db 52 ---IleSer 53
RESULT 9
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40
Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 14 Gaps: 0
DELETED1 (1-81) x US-10-194-975-40 (1-97)
Qy 1 GAATCAATCATAGTGGAGCACCACCACTACAACCCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70
RESULT 10
US-10-308-817-83
DELETED1 (1-81) x US-09-880-748-954 (1-253)
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2
Alignment Scores:
Pred. No.: 0.00774 Length: 253
Score: 93.80 Matches: 20
Percent Similarity: 80.77% Conservative: 1
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 67.00% Indels: 2
DB: 15 Gaps: 1
DELETED1 (1-81) x US-10-293-418-954 (1-253)
Qy 1 GAATCAATCATAGTGGAGCACCACCACTACAACCCGCTCTCTCAAGAGTCGGCGGAGTCAG 54
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuAsnSerArgValThrIle 69
Qy 55 AGTCAGGATATTAGCAGC 72
Db 70 SerGlnAspThrSerAsn 75
RESULT 8
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
```

```
US-10-293-418-954
; Sequence 954, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 954
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-954
```


; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-308-817-83 (1-97)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
|||||
Db 50 GlulleAsnHisSerGlySerThrAsnTyranProSerLeuLysSerArgValThr--- 68
:::

QY 61 GATATTAGC 69

Db 69 ---lleSer 70

RESULT 11

US-10-032-037B-87

; Sequence 87, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-032-037B-87 (1-97)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
|||||
Db 50 GlulleAsnHisSerGlySerThrAsnTyranProSerLeuLysSerArgValThr--- 68
:::

QY 61 GATATTAGC 69

Db 69 ---lleSer 70

RESULT 12

US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-029-988B-87 (1-97)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
|||||

Db 50 GlulleAsnHisSerGlySerThrAsnTyranProSerLeuLysSerArgValThr--- 68
:::

QY 61 GATATTAGC 69

Db 69 ---lleSer 70

RESULT 13

US-10-032-423A-87

; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-032-423A-87 (1-97)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACAAACCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
|||||

Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 14

US-10-453-698-83
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-453-698-83 (1-97)

Qy 1 GAAATCAATCATAGTGAAGCACCACCTACACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 15

US-10-029-926B-87
; Sequence 87, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.: 0.00974 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 15 Gaps: 0

DELETED1 (1-81) x US-10-029-926B-87 (1-97)

Qy 1 GAAATCAATCATAGTGAAGCACCACCTACACCGTCTCTCAAGAGTCGGCGAGTCAG 60

Db 50 GluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

Search completed: August 4, 2005, 19:56:40
Job time : 107 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:22:55 ; Search time 26 Seconds
(without alignments)
599.504 Million cell updates/sec

Title: DELETED1
Perfect score: 140
Sequence: 1 GAATCAATCATAGTGGAG.....ATATTAGCAGCTGTTAGCC 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/NOLAN463-3A/runat.04082005.120125.18808/app_query.fasta_1.263
-DB=PIR -QFMT=FASTA -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3A@cgn.1.1.63@runat.04082005.120125.18808 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 94 | 67.1 | 97 | 2 | S26806 |
| 2 | 93.9 | 67.1 | 140 | 2 | S78052 |
| 3 | 92.4 | 66.0 | 97 | 2 | S26898 |
| 4 | 92.4 | 66.0 | 97 | 2 | S26805 |
| 5 | 92.4 | 66.0 | 106 | 2 | S37454 |
| 6 | 92.4 | 66.0 | 122 | 2 | J10047 |
| 7 | 92.4 | 66.0 | 126 | 2 | S47010 |
| 8 | 92.4 | 66.0 | 133 | 2 | P80341 |
| 9 | 92.4 | 66.0 | 140 | 2 | A49045 |
| 10 | 92.4 | 66.0 | 143 | 2 | B49028 |
| 11 | 92.4 | 66.0 | 231 | 2 | B23746 |
| 12 | 88.4 | 63.1 | 97 | 2 | G34964 |
| 13 | 84.4 | 60.3 | 98 | 2 | S26905 |
| 14 | 83.4 | 59.6 | 97 | 2 | S14474 |

| | | | | | | |
|----|------|------|-----|---|--------|--------------------|
| 15 | 81.4 | 58.1 | 129 | 2 | S44114 | Ig heavy chain V r |
| 16 | 80.4 | 57.4 | 134 | 2 | S54906 | Ig heavy chain V r |
| 17 | 80 | 57.1 | 123 | 2 | S30529 | Ig heavy chain V r |
| 18 | 79.1 | 56.5 | 140 | 2 | I37782 | Ig variable region |
| 19 | 78.4 | 56.0 | 98 | 2 | S26904 | Ig heavy chain V r |
| 20 | 78.4 | 56.0 | 145 | 2 | S78055 | Ig heavy chain pre |
| 21 | 78.4 | 56.0 | 146 | 1 | GIH0H2 | Ig heavy chain pre |
| 22 | 77.4 | 55.3 | 114 | 2 | I72667 | cold agglutinin FS |
| 23 | 77.3 | 55.2 | 130 | 2 | S31673 | Ig heavy chain V r |
| 24 | 77 | 55.0 | 134 | 2 | B24672 | Ig heavy chain pre |
| 25 | 75.4 | 53.9 | 97 | 2 | JH0428 | Ig gamma chain V r |
| 26 | 74.4 | 53.1 | 106 | 2 | S26454 | Ig heavy chain V r |
| 27 | 74 | 52.9 | 116 | 2 | S38718 | Ig heavy chain V r |
| 28 | 73.4 | 52.4 | 97 | 2 | S26906 | Ig heavy chain V r |
| 29 | 73.4 | 52.4 | 97 | 2 | S12416 | Ig heavy chain V r |
| 30 | 73.4 | 52.4 | 99 | 2 | S12412 | Ig heavy chain V r |
| 31 | 73.4 | 52.4 | 105 | 2 | S44125 | Ig lambda chain V |
| 32 | 73.4 | 52.4 | 116 | 2 | B26340 | Ig heavy chain pre |
| 33 | 73.4 | 52.4 | 118 | 2 | A26340 | Ig heavy chain pre |
| 34 | 73.4 | 52.4 | 130 | 2 | S31690 | Ig heavy chain V r |
| 35 | 73.1 | 52.2 | 127 | 2 | S19668 | Ig heavy chain V r |
| 36 | 72 | 51.4 | 97 | 2 | S26804 | Ig heavy chain V r |
| 37 | 72 | 51.4 | 97 | 2 | S26808 | Ig heavy chain V r |
| 38 | 72 | 51.4 | 116 | 2 | S18557 | Ig heavy chain V r |
| 39 | 72 | 51.4 | 137 | 2 | S31676 | Ig heavy chain V r |
| 40 | 72 | 51.4 | 139 | 2 | S31696 | Ig heavy chain V r |
| 41 | 72 | 51.4 | 139 | 2 | S31586 | Ig heavy chain V r |
| 42 | 71.5 | 51.1 | 109 | 2 | PH1673 | Ig heavy chain V r |
| 43 | 71.4 | 51.0 | 97 | 2 | PL0118 | Ig heavy chain V-I |
| 44 | 71.4 | 51.0 | 98 | 2 | S26902 | Ig heavy chain V r |
| 45 | 71.4 | 51.0 | 98 | 2 | S12421 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

S26806
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26806
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26806
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WENG>
A:Cross-references: EMBL:Z14242; NID:G37716; PIDN:CAA78611.1; PID:G1335377
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 0.000731 Length: 97
Score: 94.00 Matches: 17
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 70.83% Mismatches: 4
Query Match: 67.14% Indels: 0
DB: 2 Gaps: 0

DELETED1 (1-81) x S26806 (1-97)

| | | |
|----|----|---|
| Qy | 1 | GAATCAATCATAGTGGAGCCCACTACACCCGCTCTCAAGAGTCGGCGAGTCAG 60 |
| Db | 50 | GlulileAsnHisSerGlySerThrAsnTyAsnProSerLeuIysSerArgIleThrMet 69 |
| Qy | 61 | GATATTAGCAGC 72 |
| Db | 70 | SerValAspThr 73 |

RESULT 2

S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAW>
A:Cross-references: EMBL:X5441; NID:G37815; PIDN:CAA38308.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X5441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000771 Length: 140
Score: 93.90 Matches: 21
Percent Similarity: 33.85% Conservative: 1
Best Local Similarity: 32.31% Mismatches: 2
Query Match: 67.07% Indels: 41
DB: 2 Gaps: 1

DELETED1 (1-81) x S78052 (1-140)

Qy 1 GAATCATCATAGTGGAGACCACTACACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 64 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 82
Qy 61 GATATTAGC----- 69
Db 83 ---lleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerSerValThrAla 101
Qy 70 -----AGCTGG 75
Db 102 AlaaSpThrAlaValTyTyCysAlaArgGlyGlySerValLeuArgPheLeuGluTrp 121
Qy 76 TTA 78
Db 122 Leu 122

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26898; S12420
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26898
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12363; NID:G32944; PIDN:CAA78233.1; PID:G32945
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:25111001
A:Accession: S12420

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-97 <SAN>
A:Cross-references: EMBL:X56364
C:Experimental source: V(H)4.2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00119 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x S26898 (1-97)

Qy 1 GAATCATCATAGTGGAGACCACTACACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---lleSer 70

RESULT 4
S26805
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26805
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26805
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WEN>
A:Cross-references: EMBL:Z14241; NID:G37714; PIDN:CAA78610.1; PID:G1335376
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00119 Length: 97
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x S26805 (1-97)

Qy 1 GAATCATCATAGTGGAGACCACTACACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---lleSer 70

RESULT 5
S37454
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37454
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from

A:Reference number: S37453
A:Accession: S37454
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <NCI>
A:Cross-references: EMBL:X75022; NID:G404311; PIDN:CAA52930.1; PID:G758093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Alignment Scores:
Pred. No.: 0.0012 Length: 106
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x S37454 (1-106)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 28 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 46
:::

QY 61 GATATTAGC 69

Db 47 ---IleSer 48

RESULT 6

JL0047
Ig heavy chain V region precursor (clone cR18) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C:Accession: JL0047
R:Baer, R.; Forster, A.; Lavenix, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5
A:Reference number: JL0047; MUID:88258392; PMID:3133445
A:Accession: JL0047
A:Molecule type: mRNA
A:Residues: 1-122 <BAE>
A:Experimental source: T-cell line RPMI 8402
A>Note: the authors translated the reading frame which extends to the stop codon; the se
A>Note: this sequence belongs to the VH II subgroup
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00121 Length: 122
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x JL0047 (1-122)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 58 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 76
:::

QY 61 GATATTAGC 69

Db 77 ---IleSer 78

RESULT 7

S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994

A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bir
A:Reference number: S47009
A:Accession: S47010
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00121 Length: 126
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x S47010 (1-126)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 50 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 68
:::

QY 61 GATATTAGC 69

Db 69 ---IleSer 70

RESULT 8

PS0341
Ig heavy chain V-D-J region (RAMOS) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997
C:Accession: PS0341
R:Rothen, H.
Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992
A:Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell
A:Reference number: PS0341; MUID:92171937; PMID:1540170
A:Accession: PS0341
A:Molecule type: mRNA
A:Residues: 1-133 <RAI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-38/Region: framework 1
F:39-43/Region: complementarity-determining 1
F:44-57/Region: framework 2
F:58-74/Region: complementarity-determining 2
F:75-106/Region: framework 3

Alignment Scores:
Pred. No.: 0.00121 Length: 133
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x PS0341 (1-133)

QY 1 GAAATCAATCATAGTGGAGCACCACCACTACACCCGCTCTCTCAAGAGTCGGCGAGTCAG 60
|||||
Db 58 GlulleAenHisSerGlySerThrAsnTyraenProSerLeuLysSerArgValThr--- 76
:::

QY 61 GATATTAGC 69

Db 77 ---IleSer 78

RESULT 9

A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.-C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverman, J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i b1
A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <R1>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIp:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00122 Length: 140
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x A49045 (1-140)

Qy 1 GAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 69 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 87
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 10
B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur, Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: B49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <T1M>
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIp:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00122 Length: 143
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x B49028 (1-143)

Qy 1 GAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 11

B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: B23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: B23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00125 Length: 231
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x B23746 (1-231)

Qy 1 GAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 49 GlulleAsnHisSerGlySerThrAsnTyAsnProSerLeuLysSerArgValThr--- 67
Qy 61 GATATTAGC 69
Db 68 ---IleSer 69

RESULT 12
G34964
Ig heavy chain V-IV region (Ab44) - human
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: G34964
R;Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.
J. Immunol. 142, 4054-4061, 1989
A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap
A;Reference number: A92830; MUID:89235232; PMID:2497188
A;Accession: G34964
A;Molecule type: mRNA
A;Residues: 1-97 <SAN>
A;Cross-references: UNIPROT:Q8WUX4; GB:M26998
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00404 Length: 97
Score: 88.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 63.14% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x G34964 (1-97)

Qy 1 GAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60
Db 50 GlulleAsnHisSerGlyThrAsnTyAsnProSerLeuLysSerArgValThr--- 68
Qy 61 GATATTAGC 69
Db 69 ---IleSer 70

RESULT 13
S26905
Ig heavy chain V region (DP-70 / 4.19) - human (fragment)

200

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:04:23 ; Search time 108 Seconds
(without alignments)
768.119 Million cell updates/sec

Title: DELETED1
Perfect score: 140
Sequence: 1 GAATCATCATAGTGAAG.....ATATTAGCAGCTGTTAGCC 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model
-Q=/cgn2.1/USPTO.spool.p/NOLAN463-3A/runat.04082005.120125.18797/app.query.fasta.1.263
-DB=uniprot -OPMT=fastcan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MAIRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HPAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN463-3A @CGN 1.1 244 @runat.04082005.120125.18797 -NCPU=6 -ICPU=3
-NO.MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Uniprot.03.*

1: uniprot.sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 92.4 | 66.0 | 116 | Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 2 | 92.4 | 66.0 | 595 | Q8WUX4 | Q8WUX4 homo sapien |
| 3 | 92.4 | 66.0 | 597 | Q6GMX5 | Q6GMX5 homo sapien |
| 4 | 92.4 | 66.0 | 597 | Q9BU10 | Q9BU10 homo sapien |
| 5 | 92.4 | 66.0 | 625 | Q96AA6 | Q96AA6 homo sapien |
| 6 | 86.4 | 61.7 | 597 | Q9BQB8 | Q9BQB8 homo sapien |
| 7 | 84.4 | 60.3 | 576 | Q6P4I8 | Q6P4I8 homo sapien |
| 8 | 81.3 | 58.1 | 477 | Q6GMX7 | Q6GMX7 homo sapien |
| 9 | 78.4 | 56.0 | 146 | 1 HV21 HUMAN | P06331 homo sapien |
| 10 | 73.7 | 52.6 | 139 | 2 Q86SX2 | P06331 homo sapien |
| 11 | 72.6 | 51.9 | 479 | 2 Q99M22 | Q99M22 homo sapien |
| 12 | 72 | 51.4 | 465 | 2 Q6GMX6 | Q6GMX6 homo sapien |
| 13 | 72 | 51.4 | 620 | 2 Q8EY0 | Q8EY0 homo sapien |
| 14 | 70.6 | 50.4 | 262 | 2 Q85Z11 | Q85Z11 mus musculus |
| 15 | 69.3 | 49.5 | 119 | 2 Q9UL73 | Q9UL73 homo sapien |
| 16 | 69.1 | 49.4 | 113 | 1 HV47_MOUSE | P01823 mus musculus |

| | | | | | |
|----|------|------|------|--------------|-----------------------|
| 17 | 69 | 49.3 | 116 | 1 HV61_MOUSE | P18532 mus musculus |
| 18 | 67.4 | 48.1 | 2348 | 2 Q8Z0Z7 | Q8Z0Z7 anabaena sp |
| 19 | 66.9 | 47.8 | 476 | 2 Q6GMX1 | Q6GMX1 homo sapien |
| 20 | 65 | 46.4 | 116 | 1 HV60_MOUSE | P18531 mus musculus |
| 21 | 65 | 46.4 | 478 | 2 Q6NYH3 | Q6NYH3 homo sapien |
| 22 | 64 | 45.7 | 478 | 2 Q7Z379 | Q7Z379 homo sapien |
| 23 | 60.8 | 43.4 | 3118 | 2 Q17575 | O17575 caenorhabdi |
| 24 | 59.4 | 42.4 | 150 | 2 Q95973 | Q95973 homo sapien |
| 25 | 59 | 42.1 | 136 | 2 Q6LBQ5 | Q6LBQ5 mus musculus |
| 26 | 59 | 42.1 | 137 | 1 HV46_MOUSE | P01822 mus musculus |
| 27 | 58.7 | 41.9 | 209 | 2 Q8XWU0 | Q8XWU0 ralestonia s |
| 28 | 57.5 | 41.1 | 963 | 2 Q8P5M2 | Q8P5M2 xanthomonas |
| 29 | 57.5 | 41.1 | 1160 | 1 TFC3_YEAST | P34111 saccharomyc |
| 30 | 57.4 | 41.0 | 496 | 2 Q96KX8 | Q96KX8 homo sapien |
| 31 | 57.1 | 40.8 | 163 | 2 Q84F35 | Q84F35 streptomyce |
| 32 | 56.7 | 40.5 | 212 | 2 Q926K5 | Q926K5 listeria in |
| 33 | 56.6 | 40.4 | 408 | 1 YBX0_ARATH | YBX0_ARATH arabidopsi |
| 34 | 56.4 | 40.3 | 390 | 2 Q6HH60 | Q6HH60 bacillus th |
| 35 | 56.4 | 40.3 | 545 | 2 Q6HH58 | Q6HH58 bacillus th |
| 36 | 56.4 | 40.3 | 588 | 2 Q813F9 | Q813F9 bacillus ce |
| 37 | 56.3 | 40.2 | 1177 | 2 Q82B26 | Q82B26 yersinia ps |
| 38 | 56.3 | 40.2 | 1177 | 2 Q82B26 | Q82B26 yersinia ps |
| 39 | 56 | 37.8 | 589 | 2 Q9K7H7 | Q9K7H7 bacillus ha |
| 40 | 55.9 | 39.9 | 421 | 2 Q88115 | Q88115 pseudomonas |
| 41 | 55.8 | 39.9 | 877 | 1 SEU_ARATH | Q88234 arabidopsi |
| 42 | 55.7 | 39.8 | 193 | 2 Q63FQ9 | Q63FQ9 bacillus ce |
| 43 | 55.7 | 39.8 | 193 | 2 Q73DA2 | Q73DA2 bacillus ce |
| 44 | 55.7 | 39.8 | 193 | 2 Q81HP9 | Q81HP9 bacillus ce |
| 45 | 55.7 | 39.8 | 193 | 2 Q81UW5 | Q81UW5 bacillus an |

ALIGNMENTS

RESULT 1
Q7Z3Y6
ID Q7Z3Y6 PRELIMINARY; PRT; 116 AA.
AC Q7Z3Y6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN Name=VH4-34;
GC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauning A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -.
DR HSSP; P18532; 1KCV.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;
Alignment Scores:
Pred. No.: 0.00232 Length: 116
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0
DELETED1 (1-81) x Q7Z3Y6 (1-116)
QY 1 GAATCATCATAGTGAAGCAACCACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAG 60

```
Db 50 GlulienHisSerGlySerThrAsnTyranProSerLeuLysSerArgValThr--- 68
|||
Qy 61 GATATTAGC 69
|||
Db 69 ---IleSer 70
|||

RESULT 2
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4
DT 01-MAR-2004 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
PC SEQUENCE FROM N.A.
RX TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSP; P01861; IADQ.
DR PFAM; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Alignment Scores:
Pred. No.: 0.00292 Length: 595
Score: 92.40 Matches: 19
Percent Similarity: 74.0% Conservative: 1
Best Local Similarity: 70.3% Mismatches: 1
Query Match: 66.0% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q8WUX4 (1-595)

Qy 1 GAAATCAATCATAGTGGGAAGCAACCACTACACCCGCTCTCTCAAGAGTGGCGAGTCAG 60
|||
Db 76 GlulienHisSerGlySerThrAsnTyranProSerLeuLysSerArgValThr--- 94
|||
```

```
Qy 61 GATATTAGC 69
|||
Db 95 ---IleSer 96
|||

RESULT 3
Q6GMX5 PRELIMINARY; PRT; 597 AA.
AC Q6GMX5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
PC SEQUENCE FROM N.A.
RX TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR PFAM; PF07654; CI-set; 4.
DR PFAM; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.: 0.00292 Length: 597
Score: 92.40 Matches: 19
Percent Similarity: 74.0% Conservative: 1
Best Local Similarity: 70.3% Mismatches: 1
Query Match: 66.0% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q6GMX5 (1-597)

Qy 1 GAAATCAATCATAGTGGGAAGCAACCACTACACCCGCTCTCTCAAGAGTGGCGAGTCAG 60
```

```
Db 69 GluIIeAenHisSerGlySerThrAsnTyAenProSerLeuLySerArgValThr--- 87
|||
QY 61 CATATTAGC 69
|||
Db 88 ---lleSer 89
|||

RESULT 4
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AA02963.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.: 0.00292 Length: 597
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q9BU10 (1-597)
```

```
QY 1 GAAATCAATCATAGTGGAGACCACTACACCCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
|||
Db 69 GluIIeAenHisSerGlySerThrAsnTyAenProSerLeuLySerArgValThr--- 87
|||
```

```
QY 61 CATATTAGC 69
|||
Db 88 ---lleSer 89
|||

RESULT 5
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; FG2FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.: 0.00294 Length: 625
Score: 92.40 Matches: 19
Percent Similarity: 74.07% Conservative: 1
Best Local Similarity: 70.37% Mismatches: 1
Query Match: 66.00% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q96AA6 (1-625)
```

```
QY 1 GAAATCAATCATAGTGGAGACCACTACACCCGCTCTCTCAAGAGTCGGCGGAGTCAG 60
```

```
Db 76 Glut1AenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr----- 94
Qy 61 GATATTAGC 69
Db 95 ---IleSer 96

RESULT 6
Q9BQ88 PRELIMINARY; PRT; 597 AA.
AC 05-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00290; IG-MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.: 0.0197 Length: 597
Score: 86.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 61.71% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q9BQ88 (1-597)

Qy 1 GAATCAATCATAGTGGAGCACCACCTACACCGCTCTCTCAAGAGTCGGCGAGTCAG 60
Db 69 Glut1AenHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThr--- 87
```

```
Qy 61 GATATTAGC 69
Db 88 ---IleSer 89

RESULT 7
Q6P418 PRELIMINARY; PRT; 576 AA.
AC 06P418;
AC 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE IGHM protein.
CN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 0.0371 Length: 576
Score: 84.40 Matches: 18
Percent Similarity: 70.37% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 60.29% Indels: 6
DB: 2 Gaps: 0

DELETED1 (1-81) x Q6P418 (1-576)
```

QY 1 GAATCATCATAGTGGAGACCAACCACTACAAACCGCTCTCTCAAGAGTCGGCGAGTCAG 60
 Db 77 GllullefyrHisSerGlySerThrAsnTyraSerProSerLeuLysSerArgValThr 95
 QY 61 GATATTAGC 69
 Db 96 ---lleSer 97

RESULT 8
 Q6GMX7
 ID Q6GMX7 PRELIMINARY; PRT; 477 AA.
 AC Q6GMX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073765; AAH73765.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG-MHC.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 477 AA; 51631 MW; 9PF59C09C50CFF85 CRC64;

Alignment Scores:
 Pred. No.: 0.0971 Length: 477
 Score: 81.30 Matches: 17
 Percent Similarity: 39.22% Conservative: 3
 Best Local Similarity: 33.33% Mismatches: 4
 Query Match: 58.07% Indels: 27
 DB: 2 Gaps: 1

DELETED1 (1-81) x Q6GMX7 (1-477)
 QY 4 ATCAATCATAGTGGAGACCAACCACTACAAACCGCTCTCTCAAGAGTCGGCGAGTCAG 63
 Db 70 GllullefyrHisSerGlySerThrAsnTyraSerProSerLeuLysSerArgValThr 89
 QY 64 ATT-----
 Db 90 LeuAspThrSerLysAsnGlnPheSerLeuArgLeuAsnSerValThrAlaAlaAspThr 109
 QY 67 -----AGCAGCTGG 75
 Db 110 AlaValTyrrCysAlaHisGlySerSerTrp 120

RESULT 9
 HV21_HUMAN
 ID HV21_HUMAN STANDARD; PRT; 146 AA.
 AC P06331;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
 repeat sequence in 5' flanking region.";
 RL Gene 33:181-189 (1985).
 DR PIR; A02101; G1HUH2.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
 FT DOMAIN 20 117 V segment.
 FT DOMAIN 118 127 D segment.
 FT DOMAIN 128 146 J segment.
 FT DISULFID 42 115 By similarity.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Alignment Scores:
 Pred. No.: 0.207 Length: 146
 Score: 78.40 Matches: 17
 Percent Similarity: 66.67% Conservative: 1
 Best Local Similarity: 62.96% Mismatches: 3
 Query Match: 56.00% Indels: 6
 DB: 1 Gaps: 0

DELETED1 (1-81) x HV21_HUMAN (1-146)
 QY 1 GAATCATCATAGTGGAGACCAACCACTACAAACCGCTCTCTCAAGAGTCGGCGAGTCAG 60
 Db 70 GllullefyrHisSerGlySerThrAsnTyraSerProSerLeuLysSerArgValThr 88
 QY 61 GATATTAGC 69
 Db 89 ---lleSer 90

RESULT 10
 Q86SX2

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
Alignment Scores:
Pred. No.: 1-87 Length: 465
Score: 72.00 Matches: 13
Percent Similarity: 80.00% Conservative: 3
Best Local Similarity: 65.00% Mismatches: 4
Query Match: 51.43% Indels: 0
DB: 2 Gaps: 0
DELETED1 (1-81) x Q6GMX6 (1-465)
QY 13 AGTGAAGCACCACCACTACACCGCTCTCAAGAGTCGGCGAGTCAGGATATTAGCAGC 72
|||||
Db 73 SerGlySerThrAsnTyAsnProSerLeuLysSerArgValThrMetSerValAspThr 92
|||||
RESULT 13
Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -;
DR PIR; S15590; S15590.
DR HSP; P01820; I67J.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;
Alignment Scores:
Pred. No.: 1-95 Length: 620
Score: 72.00 Matches: 13
Percent Similarity: 80.00% Conservative: 3
Best Local Similarity: 65.00% Mismatches: 4
Query Match: 51.43% Indels: 0
DB: 2 Gaps: 0
DELETED1 (1-81) x Q96EY0 (1-620)
QY 13 AGTGAAGCACCACCACTACACCGCTCTCAAGAGTCGGCGAGTCAGGATATTAGCAGC 72
|||||
Db 80 SerGlySerThrAsnTyAsnProSerLeuLysSerArgValThrMetSerValAspThr 99
|||||
RESULT 14
Q65Z11 PRELIMINARY; PRT; 262 AA.
AC Q65Z11;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-HIV-1 reverse transcriptase single-chain variable.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=96211469; PubMed=8648670;
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT by intracellular expression of single-chain variable fragments to
RT inhibit early stages of the viral life cycle.";
RL J. Virol. 70:3392-3400(1996).
DR EMBL; U48716; AAB64342.1; -;

DR GO: 0003964; F:RNA-directed DNA polymerase activity; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00408; IGC2; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS50835; IG LIKE; 2.

KW RNA-directed DNA polymerase.

SQ SEQUENCE 262 AA; 27842 MW; 7DP20138E53865E4 CRC64;

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 2.7 | Length: | 262 |
| Score: | 70.60 | Matches: | 16 |
| Percent Similarity: | 68.00% | Conservative: | 1 |
| Best Local Similarity: | 64.00% | Mismatches: | 4 |
| Query Match: | 50.43% | Indels: | 4 |
| DB: | 2 | Gaps: | 0 |

DELETED1 (1-81) x Q65Z11 (1-262)

Qy 4 ATCAATCATAGTGGGAAGCACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAGGAT 63

Db 198 IleaenTySerGlyAspThrTyTyAsnProSerLeuLysSerArgIleSer----II 216

Qy 64 ATTAGCA 70

Db 216 eThrAla 218

RESULT 15

Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus".;

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035041; AADS6277.1; -.

DR PIR; PH0876; PH0876.

DR PIR; S12416; S12416.

DR HSSP; P01820; 1G7J.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON_TER 1

FT NON_TER 119

SQ SEQUENCE 119 AA; 13219 MW; 1BDB8656420EA0BE CRC64;

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 3.66 | Length: | 119 |
| Score: | 69.30 | Matches: | 15 |
| Percent Similarity: | 37.25% | Conservative: | 4 |
| Best Local Similarity: | 29.41% | Mismatches: | 5 |
| Query Match: | 49.50% | Indels: | 27 |
| DB: | 2 | Gaps: | 1 |

DELETED1 (1-81) x Q9UL73 (1-119)

Qy 4 ATCAATCATAGTGGGAAGCACCAACTACAAACCGTCTCTCAAGAGTCGGCGAGTCAGGAT 63

Db 51 IleaenTySerGlySerThrAsnTyThrProSerLeuLysSerArgValThrIleSer 70

Qy 64 ATT----- 66

Db 71 ValAspArgSerLysAsnGlnPheSerLeuLysLeuThrSerLeuThrAlaAlaAspThr 90

Qy 67 -----AGCAGCTGG 75

Db 91 AlaValTyPheCysAlaArgLeuSerAsnTrp 101

Search completed: August 4, 2005, 19:37:58
Job time : 113 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:39:01 ; Search time 119 Seconds
(without alignments)
526.514 Million cell updates/sec

Title: DELETED2

Perfect score: 140

Sequence: 1 CGGCGGAGTCAGGATATTAG.....ACAACCCGCTCTCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3B/runat_04082005_120453_19604/app_query.fasta_1.263
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN 1.1 224 @runat_04082005_120453_19604 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRA=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : A_Geneseq 16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004as:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 100.1 | 71.5 | 253 | 5 | ABP45322 Human Bly |
| 2 | 100.1 | 71.5 | 253 | 7 | ADG96149 Single ch |
| 3 | 99.9 | 71.4 | 125 | 6 | ADA89274 Human ant |
| 4 | 98.2 | 70.1 | 80 | 2 | AAW62794 Amino aci |
| 5 | 98.2 | 70.1 | 97 | 2 | AAV05694 Multiple |
| 6 | 98.2 | 70.1 | 97 | 5 | ABG78212 Human Fv |
| 7 | 98.2 | 70.1 | 97 | 5 | ABG91903 Human ant |
| 8 | 98.2 | 70.1 | 97 | 6 | ABO27107 Human ger |
| 9 | 98.2 | 70.1 | 97 | 7 | ADH75646 Human pro |
| 10 | 98.2 | 70.1 | 97 | 7 | ADD28104 Lymphoma |

| | | | | | | |
|----|------|------|-----|---|----------|--------------------|
| 11 | 98.2 | 70.1 | 97 | 7 | ADF10048 | Adf10048 VEGF anti |
| 12 | 98.2 | 70.1 | 97 | 7 | ADF10150 | Adf10150 Antibody |
| 13 | 98.2 | 70.1 | 97 | 7 | ADF09942 | Adf09942 Antibody |
| 14 | 98.2 | 70.1 | 97 | 7 | ADJ80323 | ADJ80323 VH gene 1 |
| 15 | 98.2 | 70.1 | 114 | 3 | AB01949 | AB01949 Anti-Id1 |
| 16 | 98.2 | 70.1 | 114 | 3 | AB01950 | AB01950 Anti-Id1 |
| 17 | 98.2 | 70.1 | 114 | 3 | AB01953 | AB01953 Anti-Id1 |
| 18 | 98.2 | 70.1 | 114 | 3 | AB01959 | AB01959 High affi |
| 19 | 98.2 | 70.1 | 114 | 3 | AB01952 | AB01952 Anti-Id1 |
| 20 | 98.2 | 70.1 | 114 | 3 | AB01955 | AB01955 Streptativ |
| 21 | 98.2 | 70.1 | 114 | 3 | AB01956 | AB01956 Streptativ |
| 22 | 98.2 | 70.1 | 114 | 3 | AB01948 | AB01948 Wild-type |
| 23 | 98.2 | 70.1 | 114 | 3 | AB01954 | AB01954 Anti-Id1 |
| 24 | 98.2 | 70.1 | 114 | 7 | ADG70086 | ADG70086 Diversifi |
| 25 | 98.2 | 70.1 | 114 | 7 | ADG70013 | ADG70013 Diversifi |
| 26 | 98.2 | 70.1 | 116 | 2 | AAW66324 | AAW66324 Human imm |
| 27 | 98.2 | 70.1 | 117 | 4 | AAW60904 | AAW60904 Human bra |
| 28 | 98.2 | 70.1 | 117 | 4 | ABG55317 | ABG55317 Human liv |
| 29 | 98.2 | 70.1 | 117 | 5 | ABG43454 | ABG43454 Human pep |
| 30 | 98.2 | 70.1 | 118 | 6 | ADA89246 | ADA89246 Human ant |
| 31 | 98.2 | 70.1 | 122 | 7 | ADK17418 | ADK17418 Anti-huma |
| 32 | 98.2 | 70.1 | 122 | 8 | ADG42840 | ADG42840 scFv Abl2 |
| 33 | 98.2 | 70.1 | 123 | 2 | AAW03757 | AAW03757 Anti-rhes |
| 34 | 98.2 | 70.1 | 125 | 6 | ADA89266 | ADA89266 Human ant |
| 35 | 98.2 | 70.1 | 139 | 3 | AAV99556 | AAV99556 Human LHL |
| 36 | 98.2 | 70.1 | 139 | 6 | ABR42859 | ABR42859 Tumour-sp |
| 37 | 98.2 | 70.1 | 139 | 7 | ABW02445 | ABW02445 Human mon |
| 38 | 98.2 | 70.1 | 142 | 6 | ABP96287 | ABP96287 Anti-hrnf |
| 39 | 98.2 | 70.1 | 154 | 6 | ABP96293 | ABP96293 Human ant |
| 40 | 98.2 | 70.1 | 190 | 2 | AAV34304 | AAV34304 IGM antib |
| 41 | 98.2 | 70.1 | 202 | 2 | AAV34303 | AAV34303 IGM antib |
| 42 | 98.2 | 70.1 | 205 | 2 | AAV34299 | AAV34299 IGM antib |
| 43 | 98.2 | 70.1 | 218 | 7 | ADG70090 | ADG70090 Diversifi |
| 44 | 98.2 | 70.1 | 223 | 7 | ADJ32112 | ADJ32112 Human int |
| 45 | 98.2 | 70.1 | 224 | 7 | ADG70088 | ADG70088 Diversifi |

ALIGNMENTS

RESULT 1

ABP45322
ID ABP45322 standard; protein; 253 AA.

XX AC ABP45322;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1333.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX FN W0200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX Claim 1; Page 1993-1994; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC associated to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
XX the invention
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 0.000258 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 5 Gaps: 1

DELETED2 (1-81) x ABP45322 (1-253)

QY 3 GCGGAGTCA-----GGATAT 17
DB 26 GlyGlusSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

QY 18 TAGCAGCTGGTTAGCGAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCTCAA 77
DB 46 ----GluTrpIleGlyGluIleAsnHsSerGlySerThrAsnTyrAsnProSerLeu 64

QY 78 GAGT 81
DB 64 sSer 65

RESULT 2
ID ADG96149
XX ADG96149 standard; protein; 253 AA.
AC ADG96149;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BlyS SeqID 1333.
XX
KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
PN
XX
PD 10-JUL-2003.
XX
XX

PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BlyS), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1333; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BlyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BlyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BlyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 0.000258 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 7 Gaps: 1

DELETED2 (1-81) x ADG96149 (1-253)

QY 3 GCGGAGTCA-----GGATAT 17
DB 26 GlyGlusSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

QY 18 TAGCAGCTGGTTAGCGAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCTCAA 77
DB 46 ----GluTrpIleGlyGluIleAsnHsSerGlySerThrAsnTyrAsnProSerLeu 64

QY 78 GAGT 81
DB 64 sSer 65

RESULT 3
ID ADA89274
XX ADA89274 standard; protein; 125 AA.
AC ADA89274;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human antibody 3H2 heavy chain amino acid sequence SEQ ID NO:118.

XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003070752-A2.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-US005128.
XX
XX PR 20-FEB-2002; 2002US-0358994P.
XX
XX PA (DVAX-) DVAX CORP.
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX PI Hoogenboom HRJM, Reiter Y;
XX
XX DR WPI; 2003-663847/62.
XX N-PSDB; ADA89273.
XX
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
XX Disclosure; Fig 28B; 22app; English.
XX
XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC hTERT.
XX
XX Sequence 125 AA;
SQ
Alignment Scores:
Pred. No.: 0.000224 Length: 125
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 6 Gaps: 1
DELETED2 (1-81) x ADA89274 (1-125)
QY 3 GCGAGTACAGATATACAGC-----
Db 26 GlyGlySer-----IleSerSerSerTyrTrpAlaTrpIleArgGlnProGln 44

QY 25 -----TGTTAGCCGAATCAATCATAGTCGAAGCACTACAACTACAACTC 71
Db 44 yLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSe 64
QY 72 TCTCAAGAGT 81
Db 64 rLeuLysSer 67
RESULT 4
AAW62794
ID AAW62794 standard; peptide; 80 AA.
XX
XX AC AAW62794;
XX
XX DT 23-SEP-1998 (first entry)
XX
XX DE Amino acid sequence of a human antibody fragment.
XX
XX KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
XX OS Homo sapiens.
XX
XX PN WO9824893-A2.
XX
XX PD 11-JUN-1998.
XX
XX PF 03-DEC-1997; 97WO-US023091.
XX
XX PR 03-DEC-1996; 96US-00759620.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX FI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX WPI; 1998-333314/29.
XX
XX DR New transgenic non-human mammals - having an inactivated immunoglobulin
XX locus and a near complete human immunoglobulin locus, used for production
XX of human antibodies.
XX
XX PS Disclosure; Page 71; 128pp; English.
XX
XX CC AAW62793-822 represent fragments of human antibodies produced by
XX transgenic Xenomice, created using the method of the invention. The
XX specification describes a transgenic non-human mammal which has genome
XX modifications that comprise an inactivated endogenous immunoglobulin (Ig)
XX locus, so that the mammal does not display normal B-cell development. The
XX modified genome also has an inserted human heavy chain Ig locus in
XX germ-line configuration, the human heavy chain Ig locus comprising a human
XX micro constant region and regulatory and switch sequences, human J-H
XX genes, human D-H genes, and human V-H genes and an inserted human kappa
XX light chain Ig locus in germ-line configuration, the human kappa light
XX chain Ig locus comprising a human kappa constant region, J-kappa genes,
XX and V-kappa genes, where the number of V-H and V-kappa genes inserted are
XX selected to restore normal B-cell development in the mammal. The
XX transgenic animals have a near complete human Ig locus, including both a
XX human heavy chain locus and a human kappa light chain locus. They can be
XX used for the production of human antibodies when exposed to particular
XX antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
XX will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
XX SQ Sequence 80 AA;
Alignment Scores:
Pred. No.: 0.000334 Length: 80
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3

```
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x AAW62794 (1-80)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 42
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 62 ACAACCCGTCCTCTCAAGAGT 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 yrAsnProSerLeuLysSer 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
AAY05694
ID AAY05694 standard; protein; 97 AA.
XX AC AAY05694;
XX 19-JUL-1999 (first entry)
XX Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
DE Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
KW heavy chain variable region; VH gene; somatic hypermutation;
KW B-cell clonality; RA gene; diagnosis; human.
XX Homo sapiens.
XX FH Key Location/Qualifiers
XX Region 1..30
FT /label= FR1
FT Misc-difference 8 /note= "encoded by GGC"
FT Misc-difference 13 /note= "replaces Glu of RA"
FT Misc-difference 14 /note= "encoded by CCT"
FT Misc-difference 23 /note= "replaces Gly of RA"
FT Misc-difference 25 /note= "replaces Phe of RA"
FT Misc-difference 30 /note= "replaces Gly of RA"
FT Region 31..36
FT /label= CDR1
FT Misc-difference 31 /note= "replaces Gly of RA"
FT Misc-difference 32 /note= "replaces Phe of RA"
FT Region 37..50
FT /label= FR2
FT Region 51..66
FT /label= CDR2
FT Misc-difference 56 /note= "replaces Asn of RA"
FT Misc-difference 57 /note= "replaces Ser of RA"
FT Misc-difference 58 /note= "replaces Lys of RA"
FT Region 67..97
FT /label= FR3
FT Misc-difference 71 /note= "replaces Leu of RA"
FT Misc-difference 81 /note= "replaces Arg of RA"
XX WO9915696-A1.
XX 01-APR-1999.
XX 17-SEP-1998; 98WO-CA000873.
XX
```

```
PR 19-SEP-1997; 97CA-02216595.
PR 04-NOV-1997; 97CA-02220245.
PA (QINY/) QIN Y.
XX Qin Y;
XX WPI; 1999-276985/23.
DR N-PSDB; AAX25318.
DR
XX Determination of B-cell clonality by amplification or enzymatic
FT digestion.
XX
XX Disclosure; Fig 9D; 67pp; English.
XX
XX This sequence represents a heavy chain variable region (VH) as predicted
CC from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
CC fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
CC B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
CC in nucleotide and predicted amino acid (see AAY05691-94) sequences were
CC compared with the closest known germline VH genes; for 4d76 this was RA.
CC The results provided direct evidence that intrathecal clonally expanded B
CC -cells from the CSF of MS patients are hypermutated postgerminal centre
CC antibody-forming or memory lymphocytes that have undergone antigen
CC selection. This finding implicates an important pathogenic pathway for
CC the development of demyelination in CNS of MS. The invention provides
CC assay kits for determining B-cell or T-cell clonality. This technology
CC allows the establishment of clonal specific RNA library from pathogenic
CC cells in the CNS of patients, which is important for further
CC understanding of the role of antigen(s) in the cause of B-cell clonal
CC expansion, and towards developing antigen specific therapeutic strategy
XX
XX Sequence 97 AA;
SQ

Alignment Scores:
Pred. No.: 0.000353 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x AAY05694 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACCACT 61
   |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 62 ACAACCCGTCCTCTCAAGAGT 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 yrAsnProSerLeuLysSer 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
ABG78212
ID ABG78212 standard; protein; 97 AA.
XX
XX AC ABG78212;
XX
XX 15-NOV-2002 (first entry)
XX
XX Human Fv molecule hypervariable region related peptide #87.
KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
XX Homo sapiens.
XX
XX WO200259264-A2.
XX
XX 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US049440.
XX
```


KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.

XX Homo sapiens.

XX US2003039649-A1.

XX 27-FEB-2003.

XX 12-JUL-2002; 2002US-00194975.

XX 12-JUL-2001; 2001US-0305111P.

XX (FOOT/) FOOTE J.

XX Foote J;

XX WPI; 2003-492151/46.

XX Making humanized antibody for converting antibody, by making chimeric
 PT antibodies containing complementarity determining region from non-human
 PT antibody and appropriate framework sequences of human antibodies.

XX Example 1; Fig 1; 31pp; English.

XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies

XX Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.000353 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 6 Gaps: 0

DELETED2 (1-81) x ABO27107 (1-97)

Qy 2 GGCGAGTCAGGATATTAGCAGCTGGTTAGCGGAATCAATCATAGTGGAGACCAACT 61
 Db 42 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGTCCTCTCAAGAGT 81
 Db 59 yrAsnProSerLeuLysSer 65

RESULT 9

ADB75646

ID ADB75646 standard; protein; 97 AA.

XX

AC ADB75646;

XX 04-DEC-2003 (first entry)
 DT Human protein relating to the invention SEQ ID NO:55.
 XX antibody library; CD1 region; CD2 region; VH region; VL region;
 KW immunoglobulin; CD3 region; TM1 scFv; human.
 XX Homo sapiens.

XX WO2003044198-A1.

XX 30-MAY-2003.

XX 22-NOV-2002; 2002WO-JP012236.

XX 22-NOV-2001; 2001JP-00358602.

XX (UYKE-) UNIV KEIO.

XX Shimizu N, Takayanagi A, Okui M;

XX WPI; 2003-449818/42.

XX Highly stable artificial antibody libraries with super-repository and
 PT little contamination from unexpressible ones, useful as tool in
 PT proteomics and e.g. for diagnosis and treating various diseases.

XX Disclosure; Page 101; 108pp; Japanese.

XX The invention relates to a novel artificial single-stranded antibody
 CC library with superior-repository. The library is created by using a cDNA
 CC library as template for amplifying a fragment containing the CD1 and CD2
 CC regions of the VH or VL region of immunoglobulin gene and a fragment
 CC containing the CD3 region by PCR, respectively, producing VH and VL
 CC libraries, transferring into a host, and displaying the single-stranded
 CC antibody on a phage surface. An antibody library of the invention is
 CC useful as a tool in proteomics and antibody chips and filters, for
 CC screening ligands for antigens, and for studying protein-DNA interaction,
 CC diagnosis and treating various diseases. The present sequence represents
 CC a protein of the invention.

XX Sequence 97 AA;

Alignment Scores:
 Pred. No.: 0.000353 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 7 Gaps: 0

DELETED2 (1-81) x ADB75646 (1-97)

Qy 2 GGCGAGTCAGGATATTAGCAGCTGGTTAGCGGAATCAATCATAGTGGAGACCAACT 61
 Db 42 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGTCCTCTCAAGAGT 81
 Db 59 yrAsnProSerLeuLysSer 65

RESULT 10

ADD28104

ID ADD28104 standard; protein; 97 AA.

XX

AC ADD28104;

DT 15-JAN-2004 (first entry)

XX

DE Lymphoma related immunoglobulin variable region F5.

XX

KW B-cell; malignant; immunoglobulin; immunoglobulin variable region;

KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
 KW cyclostatic; gene therapy; glycosylation inhibitor;
 KW non-Hodgkin's lymphoma.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO20003074059-A2.
 XX
 XX PD 12-SEP-2003.
 XX
 XX PF 24-FEB-2003; 2003WO-GB000783.
 XX
 XX PR 07-MAR-2002; 2002GB-00005395.
 XX
 XX PA (CANC-) CANCER RES TECHNOLOGY LTD.
 XX
 XX PI Zhu D, Stevenson F;
 XX PI WPI; 2003-902720/82.
 DR
 XX
 XX
 PT Classifying a B-cell as malignant or normal by isolating a sequence
 PT representing an Ig variable region from the B cell, detecting the
 PT presence of a glycosylation site and classifying the cell as malignant or
 PT normal.
 XX
 XX Disclosure; Fig 4; 61pp; English.
 PS
 XX
 XX The present invention describes a method for classifying a B-cell as
 CC malignant or normal comprising: (a) isolating a sequence representing an
 CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the
 CC presence of a glycosylation site; and (c) classifying the cell as
 CC malignant or normal on the basis of the presence or absence of a
 CC glycosylation site. Also described: (1) treating a patient suffering from
 CC or at risk of having lymphoma; (2) screening for substances capable of
 CC inhibiting glycosylation of the Ig variable region of the B cell receptor
 CC ; and (3) screening for substances (S) capable of inhibiting the
 CC interaction between letins of the type found in the germinal centre and
 CC N-glycans found on the surface of Ig of lymphoma cells. (S) has
 CC cyclostatic activity, and can be used in gene therapy, and as a
 CC glycosylation inhibitor. The method is useful in classifying a B-cell as
 CC malignant or normal. The glycosylation inhibitor is useful in preparing a
 CC medicament for treating non-Hodgkin's lymphoma. The present sequence
 CC represents an Ig variable region sequence which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 97 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0.000353 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 7 Gaps: 0
 DELETED2 (1-81) x ADD28104 (1-97)
 Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCGGAATCAATCATAGTCGAGCACCACACT 61
 Db 42 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGCTCTCAAGAGT 81
 Db 59 yRAEnProSerLeuLysSer 65
 RESULT 11
 ADF10048
 ID ADF10048 standard; protein; 97 AA.
 XX
 AC ADF10048;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Antibody heavy chain variable region VH_4-34.

XX VEGF antibody heavy chain variable region VH_4-34.
 DE
 XX Antibody; stability; solubility; antigen binding affinity;
 KW variable region; human; VEGF.
 XX
 XX Homo sapiens.
 OS
 XX WO20003074679-A2.
 XX
 XX PD 12-SEP-2003.
 XX
 XX PF 03-MAR-2003; 2003WO-US006598.
 XX
 XX PR 01-MAR-2002; 2002US-0360843P.
 XX PR 29-MAY-2002; 2002US-0384197P.
 XX
 XX (XENC-) XENCOR.
 XX
 XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
 PI WPI; 2003-722066/68.
 DR
 XX
 XX Computer optimization of physicochemical properties of antibodies
 PT comprises analyzing the interactions of amino acids at variable
 PT positions.
 XX
 XX Example 6; Fig 16a; 135pp; English.
 PS
 XX
 XX The present invention relates to a method for optimizing at least one
 CC physico-chemical property of an antibody by a computational screening
 CC method. The method comprises: receiving a template antibody structure;
 CC selecting at least one variable position belonging to the antibody
 CC structure; selecting at least one amino acid to be considered at the
 CC variable position(s); analyzing the interaction of each selected amino
 CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one
 CC optimized physico-chemical property. The method is useful for optimizing
 CC the physico-chemical properties of an antibody, especially the stability,
 CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.
 XX
 XX Sequence 97 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0.000353 Length: 97
 Score: 98.20 Matches: 19
 Percent Similarity: 65.62% Conservative: 2
 Best Local Similarity: 59.38% Mismatches: 3
 Query Match: 70.14% Indels: 8
 DB: 7 Gaps: 0
 DELETED2 (1-81) x ADF10048 (1-97)
 Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCGGAATCAATCATAGTCGAGCACCACACT 61
 Db 42 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
 Qy 62 ACAACCCGCTCTCAAGAGT 81
 Db 59 yRAEnProSerLeuLysSer 65
 RESULT 12
 ADF10150
 ID ADF10150 standard; protein; 97 AA.
 XX
 AC ADF10150;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Antibody heavy chain variable region VH_4-34.

| | |
|-----------------------------------|---|
| XX | WO2003048321-A2. |
| PN | 12-JUN-2003. |
| XX | |
| XX | 03-DEC-2002; 2002WO-US038450. |
| PP | |
| XX | 03-DEC-2001; 2001US-0336591P. |
| PR | (ALEX-) ALEXION PHARM INC. |
| XX | |
| PA | Rother R, Wu D; |
| PI | |
| XX | WPI; 2003-513753/48. |
| DR | |
| XX | Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody. |
| PT | |
| PT | |
| PT | |
| XX | Disclosure; SEQ ID NO 83; 77pp; English. |
| PS | |
| CC | The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the sequence of the first component to sequencers contained in a reference database of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different than the first component, the second component selected from the group consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the second component to sequences contained in a reference database of antibody sequences or antibody fragment sequences from the target species; (viii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the VH gene locus. |
| CC | |
| XX | Sequence 97 AA; |
| SQ | |
| Alignment Scores: | |
| Pred. No.: | Length: 97 |
| Score: | 98.20 Matches: 19 |
| Percent Similarity: | Conservative: 2 |
| Best Local Similarity: | Mismatches: 3 |
| Query Match: | Indels: 8 |
| DB: | Gaps: 0 |
| DELETED2 (1-81) x ADJ80323 (1-97) | |
| QY | 2 GGGCGAGTCAGCATATTAGCAGCTGGTTAGCCGAAATCAATCATGTGGAAGCACCAACT 61 : |
| Db | 42 GlyLys----GlyLeu---GlutPrleGlyGlulleAsnHisSerGlySerThrAsnt 59 :: |
| QY | 62 ACAACCCGTCCTCTCAAGAGT 81 |
| Db | 59 yrAsnProSerLeuLysSer 65 |
| RESULT 15 | |
| AAB01949 | |
| ID | AAB01949 standard; protein; 114 AA. |
| XX | |

| | | | |
|------------------------|--------|---------------|----|
| Score: | 98.20 | Matches: | 19 |
| Percent Similarity: | 65.62% | Conservative: | 2 |
| Best Local Similarity: | 59.38% | Mismatches: | 3 |
| Query Match: | 70.14% | Indels: | 8 |
| DB: | 3 | Gaps: | 0 |

DELETED2 (1-81) x AAB01949 (1-114)

[illegible]

Search completed: August 4, 2005, 20:00:48
Job time : 123 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:53:13 ; Search time 29.5 Seconds

(without alignments)

409.937 Million cell updates/sec

Title:

DELETED2

Perfect score: 140

Sequence: 1 CGGCGGAGTCAGGATATTAG.....ACAACCCGTCCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/NOLAN463-3B/runat 04082005 120454 19634/app query.fasta_1.263
-DB=Issued Patents AA -QWTF=fastan -SUFFIX=xai -MINWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN 1 1 46 @runat 04082005 120454 19634 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 98.2 | 70.1 | 116 | 3 | US-08-545-809A-118 |
| 2 | 98.2 | 70.1 | 123 | 3 | US-08-793-450-4 |
| 3 | 98.2 | 70.1 | 139 | 4 | US-09-203-768A-2 |
| 4 | 98.2 | 70.1 | 472 | 3 | US-08-793-450-8 |
| 5 | 93.2 | 66.6 | 429 | 4 | US-09-372-425A-6 |
| 6 | 92.1 | 65.8 | 118 | 3 | US-09-025-769B-25 |
| 7 | 92.1 | 65.8 | 118 | 4 | US-09-490-070A-25 |
| 8 | 92.1 | 65.8 | 118 | 4 | US-09-490-153-25 |
| 9 | 92.1 | 65.8 | 118 | 4 | US-09-490-324-25 |
| 10 | 91.1 | 65.1 | 120 | 3 | US-08-545-809A-137 |
| 11 | 87.2 | 62.3 | 147 | 4 | US-09-471-276-835 |
| 12 | 86.3 | 61.6 | 130 | 3 | US-08-466-151-5 |

| | | | | | | |
|----|------|------|-----|---|--------------------|--------------------|
| 13 | 86.3 | 61.6 | 130 | 3 | US-08-466-163B-5 | Sequence 5, Appli |
| 14 | 86.3 | 61.6 | 130 | 4 | US-09-802-096-5 | Sequence 5, Appli |
| 15 | 86.3 | 61.6 | 130 | 4 | US-09-802-077-5 | Sequence 5, Appli |
| 16 | 85.2 | 60.9 | 447 | 4 | US-09-372-425A-2 | Sequence 2, Appli |
| 17 | 83.1 | 59.4 | 118 | 2 | US-08-652-816A-13 | Sequence 13, Appli |
| 18 | 83.1 | 59.4 | 139 | 4 | US-09-471-276-837 | Sequence 837, App |
| 19 | 83.1 | 59.4 | 244 | 3 | US-08-918-148-79 | Sequence 79, Appli |
| 20 | 83.1 | 59.4 | 244 | 3 | US-08-918-148-79 | Sequence 79, Appli |
| 21 | 81.2 | 58.0 | 119 | 5 | US-08-428-137-16 | Sequence 16, Appli |
| 22 | 81.2 | 58.0 | 119 | 5 | PCT-US93-10555-16 | Sequence 16, Appli |
| 23 | 80.1 | 57.2 | 100 | 4 | US-09-726-219A-169 | Sequence 169, App |
| 24 | 80.1 | 57.2 | 117 | 4 | US-09-720-493-2 | Sequence 2, Appli |
| 25 | 79.3 | 56.6 | 100 | 2 | US-08-273-146-69 | Sequence 69, Appli |
| 26 | 79.3 | 56.6 | 137 | 3 | US-08-466-163B-7 | Sequence 7, Appli |
| 27 | 79.3 | 56.6 | 137 | 3 | US-08-466-163B-7 | Sequence 7, Appli |
| 28 | 79.3 | 56.6 | 137 | 4 | US-09-802-096-7 | Sequence 7, Appli |
| 29 | 79.3 | 56.6 | 137 | 4 | US-09-802-077-7 | Sequence 7, Appli |
| 30 | 79.1 | 56.5 | 119 | 3 | US-09-025-769B-39 | Sequence 39, Appli |
| 31 | 79.1 | 56.5 | 119 | 3 | US-09-025-769B-65 | Sequence 65, Appli |
| 32 | 79.1 | 56.5 | 119 | 4 | US-09-490-070A-39 | Sequence 39, Appli |
| 33 | 79.1 | 56.5 | 119 | 4 | US-09-490-070A-65 | Sequence 65, Appli |
| 34 | 79.1 | 56.5 | 119 | 4 | US-09-490-153-39 | Sequence 39, Appli |
| 35 | 79.1 | 56.5 | 119 | 4 | US-09-490-153-65 | Sequence 65, Appli |
| 36 | 79.1 | 56.5 | 119 | 4 | US-09-490-324-39 | Sequence 39, Appli |
| 37 | 79.1 | 56.5 | 119 | 4 | US-09-490-324-65 | Sequence 65, Appli |
| 38 | 78.3 | 55.9 | 118 | 4 | US-09-343-698-6 | Sequence 6, Appli |
| 39 | 78.3 | 55.9 | 118 | 4 | US-08-325-955-6 | Sequence 6, Appli |
| 40 | 78.3 | 55.9 | 119 | 3 | US-08-767-128-18 | Sequence 18, Appli |
| 41 | 78.3 | 55.9 | 213 | 4 | US-09-170-769A-2 | Sequence 2, Appli |
| 42 | 78.3 | 55.9 | 832 | 3 | US-08-630-820-7 | Sequence 7, Appli |
| 43 | 78.3 | 55.9 | 832 | 4 | US-09-273-453-7 | Sequence 7, Appli |
| 44 | 78.1 | 55.8 | 116 | 3 | US-08-545-809A-140 | Sequence 140, App |
| 45 | 77.9 | 55.6 | 76 | 3 | US-08-851-362D-22 | Sequence 22, Appli |

ALIGNMENTS

RESULT 1

US-08-545-809A-118

; Sequence 118, Application US/08545809A

; Patent No. 6096878

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku

; APPLICANT: Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 145

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A

; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP93/00603

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29, 066

; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 118:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-118

Alignment Scores:

Pred. No.: 4.16e-05 Length: 116
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 3 Gaps: 0

DELETED2 (1-81) x US-08-545-809A-118 (1-116)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCAACT 61
Db 61 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 78 yrAsnProSerLeuLysSer 84

RESULT 2

US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-4

Alignment Scores:

Pred. No.: 4.25e-05 Length: 123
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 3 Gaps: 0

DELETED2 (1-81) x US-08-793-450-4 (1-123)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCAACT 61
Db 42 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yrAsnProSerLeuLysSer 65

RESULT 3

US-09-203-768A-2
; Sequence 2, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-2

Alignment Scores:

Pred. No.: 4.45e-05 Length: 139
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 4 Gaps: 0

DELETED2 (1-81) x US-09-203-768A-2 (1-139)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCAACT 61
Db 61 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 78 yrAsnProSerLeuLysSer 84

RESULT 4

US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 472 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-793-450-8

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 6,98e-05 | Length: | 472 |
| Score: | 98.20 | Matches: | 19 |
| Percent Similarity: | 65.62% | Conservative: | 2 |
| Best Local Similarity: | 59.38% | Mismatches: | 3 |
| Query Match: | 70.14% | Indels: | 8 |
| DB: | 3 | Gaps: | 0 |

DELETED2 (1-81) x US-08-793-450-8 (1-472)

QY 2 GGGCGAGTCAGATATTAGCAGCTGGTTCAGCGAATCAATCATAGTCGAGACCAACT 61

Db 61 GlyLys----GlyLeu----GlutPileGlyGluileAsnHisSerGlySerThrAsnt 78

QY 62 ACAACCCGCTCTCTCAAGAGT 81

Db 78 yRAsnProSerLeuLysSer 84

RESULT 5

US-09-372-425A-6

Sequence 6, Application US/09372425A

Patent No. 6475749

GENERAL INFORMATION:

APPLICANT: Sherie L. Morrison

APPLICANT: Ramon Montano

TITLE OF INVENTION: Improved Rh Antibody

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Oppenheimer Wolff & Donnelly LLP

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 98

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/372,425A

FILING DATE: August 11, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Oldenakmp, David J.

REGISTRATION NUMBER: 29,421

REFERENCE/DOCKET NUMBER: 510015-223

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 788-5100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 429 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Heavy chain without Tailpiece - AA

US-09-372-425A-6

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 0.00033 | Length: | 429 |
| Score: | 93.20 | Matches: | 18 |
| Percent Similarity: | 65.62% | Conservative: | 3 |
| Best Local Similarity: | 56.25% | Mismatches: | 3 |
| Query Match: | 66.57% | Indels: | 8 |
| DB: | 4 | Gaps: | 0 |

DELETED2 (1-81) x US-09-372-425A-6 (1-429)

QY 2 GGGCGAGTCAGATATTAGCAGCTGGTTCAGCGAATCAATCATAGTCGAGACCAACT 61

Db 61 GlyLys----GlyLeu----GlutPileGlyGluileAsnHisSerGlySerThrAsnt 78

QY 62 ACAACCCGCTCTCTCAAGAGT 81

Db 78 yRAsnProSerLeuLysSer 84

RESULT 6

US-09-025-769B-25

Sequence 25, Application US/09025769B

Patent No. 630064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-09-025-769B-25

Alignment Scores:
Pred. No.: 0.000291 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: Gaps: 1

DELETED2 (1-81) x US-09-025-769B-25 (1-118)
Qy 3 GCGAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysG1 44
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGGAAGCACCAACTACAAACCGTCTCTCAA 77
Db 44 yLeuGlutrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
Qy 78 GAGT 81
Db 64 sSer 65

RESULT 7
US-09-490-070A-25
; Sequence 25, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-09-490-070A-25

Alignment Scores:
Pred. No.: 0.000291 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: Gaps: 1

DELETED2 (1-81) x US-09-490-070A-25 (1-118)
Qy 3 GCGAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysG1 44
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGGAAGCACCAACTACAAACCGTCTCTCAA 77
Db 44 yLeuGlutrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
Qy 78 GAGT 81
Db 64 sSer 65

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-070A-25

Alignment Scores:
Pred. No.: 0.000291 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: Gaps: 1

DELETED2 (1-81) x US-09-490-070A-25 (1-118)
Qy 3 GCGAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerTyrTyrTrpSerTrpIleArgGlnProProGlyLysG1 44
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGGAAGCACCAACTACAAACCGTCTCTCAA 77
Db 44 yLeuGlutrpIleGlyGluIleTyrHisSerGlySerThrAsnTyrAsnProSerLeuLy 64
Qy 78 GAGT 81
Db 64 sSer 65

RESULT 8
US-09-490-153-25
; Sequence 25, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-153-25

Alignment Scores:
Pred. No.: 0.000291 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: 4 Gaps: 1

DELETED2 (1-81) x US-09-490-153-25 (1-118)

QY 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----lleSerSerTyTrpSerTrpIleArgGlnProProGlyLysG1 44
QY 25 -----TGGTTAGCGGAAATCAATCATAGTGGAGACCAACTACAACCGTCTCTCAA 77
Db 44 YleuGluTrpIleGlyGluIleTyHisSerGlySerThrAsnTyAsnProSerLeuY 64
QY 78 GAGT 81
Db 64 sSer 65

RESULT 9
US-09-490-324-25
; Sequence 25, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-137
```

```
;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-490-324-25

Alignment Scores:
Pred. No.: 0.000291 Length: 118
Score: 92.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 65.79% Indels: 19
DB: 4 Gaps: 1

DELETED2 (1-81) x US-09-490-324-25 (1-118)

QY 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----lleSerSerTyTrpSerTrpIleArgGlnProProGlyLysG1 44
QY 25 -----TGGTTAGCGGAAATCAATCATAGTGGAGACCAACTACAACCGTCTCTCAA 77
Db 44 YleuGluTrpIleGlyGluIleTyHisSerGlySerThrAsnTyAsnProSerLeuY 64
QY 78 GAGT 81
Db 64 sSer 65

RESULT 10
US-08-545-809A-137
; Sequence 137, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-137
```

```
Alignment Scores:
Pred. No.: 0.000402 Length: 120
Score: 91.10 Matches: 20
Percent Similarity: 52.27% Conservative: 3
Best Local Similarity: 45.45% Mismatches: 2
Query Match: 65.07% Indels: 19
DB: 3 Gaps: 1

DELETED2 (1-81) x US-08-545-809A-137 (1-120)

Qy 3 GCGGAGTCAGGATATTAGCAGC----- 24
Db 45 GlyAspSer-----lleSerSerGlyAsnTrpValArgGlnProProGlyLysG1 63
Qy 25 -----TGGTTAGCCGAATCAATCATAGTGGAGCACCACCACTACACCGCTCTCTCAA 77
Db 63 yLeuGluTrpIleGlyGluIleHisHisSerGlySerThrTrpTrpAsnProSerLeuLy 83
Qy 78 GAGT 81
Db 83 sser 84

RESULT 11
US-09-471-276-835
; Sequence 835, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 835
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26...-1
US-09-471-276-835

Alignment Scores:
Pred. No.: 0.0015 Length: 147
Score: 87.20 Matches: 16
Percent Similarity: 65.62% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 62.29% Indels: 8
DB: 4 Gaps: 0

DELETED2 (1-81) x US-09-471-276-835 (1-147)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTAGCGGAATCAATCATAGTGGAGCACCACACT 61
Db 69 GlyLys---GlyLeu---GluTrpIleSerGluIleAspHisGlyGlyAsnThrAsnT 86
Qy 62 ACAACCGCTCTCTCAAGAGT 81
Db 86 yfAsnProSerLeuLysSer 92

RESULT 12
US-08-466-151-5
; Sequence 5, Application US/08466151
```

```
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G. Immunoglobulin Variants
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-5

Alignment Scores:
Pred. No.: 0.0019 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 3 Gaps: 1

DELETED2 (1-81) x US-08-466-151-5 (1-130)

Qy 1 CCGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuSerLeuThrCysThrValThrGlyTyrThrIleThrSerAsp 32
Qy 22 -----AGCTGGTTAGCCGAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
Qy 40 AATCATAGTGGAGCACCACCACTACACCGCTCTCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSeryTrpAsnProSerLeuLysSer 66

RESULT 13
```



```
US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Alignment Scores:
Pred. No.: 0.0019 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 3 Gaps: 1

DELETED2 (1-81) x US-08-466-163B-5 (1-130)
Qy 1 CGGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrIleThrSerAsp 32
Qy 22 -----AGCTGGTTAGCCGAAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
Qy 40 AATCATAGTGAAGACCACTACAAACCGCTCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 14
US-08-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-802-096-5

Alignment Scores:
Pred. No.: 0.0019 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 3 Gaps: 1

DELETED2 (1-81) x US-08-466-163B-5 (1-130)
Qy 1 CGGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrIleThrSerAsp 32
Qy 22 -----AGCTGGTTAGCCGAAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
Qy 40 AATCATAGTGAAGACCACTACAAACCGCTCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 14
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Alignment Scores:
Pred. No.: 0.0019 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 4 Gaps: 1

DELETED2 (1-81) x US-09-802-096-5 (1-130)
Qy 1 CGGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrIleThrSerAsp 32
Qy 22 -----AGCTGGTTAGCCGAAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
Qy 40 AATCATAGTGAAGACCACTACAAACCGCTCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66

RESULT 15
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Alignment Scores:
Pred. No.: 0.0019 Length: 130
Score: 86.30 Matches: 17
Percent Similarity: 40.74% Conservative: 5
Best Local Similarity: 31.48% Mismatches: 5
Query Match: 61.64% Indels: 27
DB: 4 Gaps: 1

DELETED2 (1-81) x US-09-802-077-5 (1-130)
Qy 1 CGGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnSerLeuThrCysThrValThrGlyThrIleThrSerAsp 32
Qy 22 -----AGCTGGTTAGCCGAAATC 39
Db 33 AsnAlaTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 52
Qy 40 AATCATAGTGAAGACCACTACAAACCGCTCTCAAGAGT 81
Db 53 AsnHisSerGlyThrThrSerTyrAsnProSerLeuLysSer 66
```

Search completed: August 4, 2005, 20:06:46
Job time : 31.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 20:04:58 ; Search time 105.5 Seconds
(without alignments)
599.473 Million cell updates/sec

Title:

Perfect score: 140

Sequence:

1 CGGCGAGTCAGGATATTAG.....ACAACCCGTCCTCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 3505720

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/p/NOLAN463-3B/runat_04082005_120456_19700/app_query.fasta_1.263
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -WINMATCH=0.1
-LOOPCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=NOLAN463-3B @CGN 1.1 199 @runat 04082005_120456_19700
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1
-FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 100.1 | 71.5 | 253 | 10 | US-09-880-748-1333 |
| 2 | 100.1 | 71.5 | 253 | 15 | US-10-293-418-1333 |
| 3 | 99.9 | 71.4 | 125 | 15 | US-10-371-942-118 |
| 4 | 98.2 | 70.1 | 80 | 14 | US-10-078-958-2 |
| 5 | 98.2 | 70.1 | 97 | 14 | US-10-194-975-40 |
| 6 | 98.2 | 70.1 | 97 | 15 | US-10-308-817-83 |
| 7 | 98.2 | 70.1 | 97 | 15 | US-10-032-037B-87 |
| 8 | 98.2 | 70.1 | 97 | 15 | US-10-029-988B-87 |
| 9 | 98.2 | 70.1 | 97 | 15 | US-10-032-423A-87 |
| 10 | 98.2 | 70.1 | 97 | 15 | US-10-453-698-83 |
| 11 | 98.2 | 70.1 | 97 | 15 | US-10-029-926B-87 |
| 12 | 98.2 | 70.1 | 97 | 16 | US-10-379-392-47 |
| 13 | 98.2 | 70.1 | 114 | 17 | US-10-733-532-128 |
| 14 | 98.2 | 70.1 | 115 | 17 | US-10-898-408-12 |
| 15 | 98.2 | 70.1 | 117 | 9 | US-09-884-761-44315 |
| 16 | 98.2 | 70.1 | 118 | 15 | US-10-371-942-90 |
| 17 | 98.2 | 70.1 | 118 | 17 | US-10-893-576-192 |
| 18 | 98.2 | 70.1 | 122 | 15 | US-10-360-828-63 |
| 19 | 98.2 | 70.1 | 125 | 15 | US-10-371-942-110 |
| 20 | 98.2 | 70.1 | 139 | 14 | US-10-300-675-2 |
| 21 | 98.2 | 70.1 | 139 | 17 | US-10-310-124-2 |
| 22 | 98.2 | 70.1 | 139 | 17 | US-10-893-576-43 |
| 23 | 98.2 | 70.1 | 142 | 17 | US-10-484-790A-10 |
| 24 | 98.2 | 70.1 | 223 | 10 | US-09-972-656-66 |
| 25 | 98.2 | 70.1 | 229 | 10 | US-09-972-656-82 |
| 26 | 98.2 | 70.1 | 230 | 10 | US-09-972-656-72 |
| 27 | 98.2 | 70.1 | 249 | 10 | US-09-880-748-1321 |
| 28 | 98.2 | 70.1 | 249 | 15 | US-10-293-418-1321 |
| 29 | 98.2 | 70.1 | 250 | 10 | US-09-880-748-1413 |
| 30 | 98.2 | 70.1 | 250 | 15 | US-10-293-418-1413 |
| 31 | 98.2 | 70.1 | 254 | 10 | US-09-880-748-1659 |
| 32 | 98.2 | 70.1 | 254 | 15 | US-10-293-418-1659 |
| 33 | 98.2 | 70.1 | 450 | 17 | US-10-484-790A-17 |
| 34 | 98.2 | 70.1 | 453 | 17 | US-10-484-790A-18 |
| 35 | 97.2 | 69.4 | 249 | 10 | US-09-880-748-957 |
| 36 | 97.2 | 69.4 | 249 | 15 | US-10-293-418-957 |
| 37 | 95 | 67.9 | 246 | 10 | US-09-880-748-1847 |
| 38 | 95 | 67.9 | 246 | 15 | US-10-293-418-1847 |
| 39 | 94.2 | 67.3 | 123 | 14 | US-10-269-805-31 |
| 40 | 94.2 | 67.3 | 123 | 14 | US-10-269-805-55 |
| 41 | 94.2 | 67.3 | 255 | 10 | US-09-880-748-1642 |
| 42 | 94.2 | 67.3 | 255 | 15 | US-10-293-418-1642 |
| 43 | 93.7 | 66.9 | 116 | 15 | US-10-308-817-189 |
| 44 | 93.7 | 66.9 | 116 | 15 | US-10-453-698-189 |
| 45 | 93.2 | 66.6 | 250 | 10 | US-09-880-748-993 |

ALIGNMENTS

RESULT 1
US-09-880-748-1333
; Sequence 1333, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: 2001-06-15
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

```
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.: 0.000755 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 1 Gaps: 1

DELETED2 (1-81) x US-09-880-748-1333 (1-253)

QY 3 GCGAGTCA-----GGATAT 17
   |||||
Db 26 GlyGluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
   |||||
QY 18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAA 77
   |||::: |||||
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLy 64
   |||||
QY 78 GAGT 81
   ||||
Db 64 sSer 65

RESULT 3
US-10-371-942-118
; Sequence 118, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-118

Alignment Scores:
Pred. No.: 0.000704 Length: 125
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 15 Gaps: 1

DELETED2 (1-81) x US-10-371-942-118 (1-125)

QY 3 GCGAGTCAAGTATTAGCAGC----- 24
   |||||
Db 26 GlyGlySer-----IleSerSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44
   |||||
QY 25 -----TGGTTAGCCGAAATCAATCATAGTGGAGACCAACTACAAACCGTC 71
   |||::: |||||
Db 44 YLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyraAsnProSe 64
   |||||
QY 72 TCTCAAGT 81
   |||||
Db 64 rLeuLysSer 67

RESULT 4
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS, HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
```

```
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1333

Alignment Scores:
Pred. No.: 0.000755 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 1 Gaps: 1

DELETED2 (1-81) x US-09-880-748-1333 (1-253)

QY 3 GCGAGTCA-----GGATAT 17
   |||||
Db 26 GlyGluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45
   |||||
QY 18 TAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGACCAACTACAAACCGTCTCTCAA 77
   |||::: |||||
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyraAsnProSerLeuLy 64
   |||||
QY 78 GAGT 81
   ||||
Db 64 sSer 65

RESULT 2
US-10-293-418-1333
; Sequence 1333, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.: 0.000755 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 15 Gaps: 1

DELETED2 (1-81) x US-10-293-418-1333 (1-253)
```

; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-2

Alignment Scores:
Pred. No.: 0.00107 Length: 80
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 14 Gaps: 0

DELETED2 (1-81) x US-10-078-958-2 (1-80)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAAGCACCACCAACT 61
Db 25 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 42
QY 62 ACAACCCGCTCTCTCAAGAGT 81
Db 42 yRAsnProSerLeuLysSer 48

RESULT 5

US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIORITY FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 14 Gaps: 0

DELETED2 (1-81) x US-10-194-975-40 (1-97)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAAGCACCACCAACT 61
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 59
QY 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yRAsnProSerLeuLysSer 65

RESULT 6

US-10-308-817-83
; Sequence 83, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37

; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-308-817-83

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-308-817-83 (1-97)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAAGCACCACCAACT 61
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 59
QY 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yRAsnProSerLeuLysSer 65

RESULT 7

US-10-032-037B-87
; Sequence 87, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-87

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-032-037B-87 (1-97)

QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAAGCACCACCAACT 61
Db 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnt 59
QY 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yRAsnProSerLeuLysSer 65

RESULT 8

US-10-029-988B-87
; Sequence 87, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

```
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-87

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-029-988B-87 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAGACCAACT 61
Db 42 GlyLys----GlyLeu-----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 9
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-032-423A-87 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAGACCAACT 61
Db 42 GlyLys----GlyLeu-----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 10
US-10-032-423A-87
; Sequence 87, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-87

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-032-423A-87 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAGACCAACT 61
Db 42 GlyLys----GlyLeu-----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65
```

```
US-10-453-698-83
; Sequence 83, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-453-698-83

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-453-698-83 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAGACCAACT 61
Db 42 GlyLys----GlyLeu-----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 11
US-10-029-926B-87
; Sequence 87, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-87

Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 15 Gaps: 0

DELETED2 (1-81) x US-10-029-926B-87 (1-97)
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTCGAGACCAACT 61
Db 42 GlyLys----GlyLeu-----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65
```

```
RESULT 12
US-10-379-392-47
; Sequence 47, Application US/10739392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-47
Alignment Scores:
Pred. No.: 0.00111 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 16 Gaps: 0

DELETED2 (1-81) x US-10-379-392-47 (1-97)
Qy 2 GGCGAGTCAGCATATTAGCAGCTGGTTAGCCGAATCAATCATAGTCGAAGCACCACCACT 61
Db 42 GlyLys----GlyLeu----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yrasnProSerLeuLysSer 65

RESULT 13
US-10-733-532-128
; Sequence 128, Application US/10733532
; Publication No. US20050026246A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2002B
; CURRENT APPLICATION NUMBER: US/10/733,532
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: PCT/G802/02688
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 10/146,505
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-532-128
Alignment Scores:
Pred. No.: 0.00115 Length: 114
Score: 99.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
```

```
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 17 Gaps: 0

DELETED2 (1-81) x US-10-733-532-128 (1-114)
Qy 2 GGCGAGTCAGCATATTAGCAGCTGGTTAGCCGAATCAATCATAGTCGAAGCACCACCACT 61
Db 36 GlyLys----GlyLeu----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 53
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 53 yrasnProSerLeuLysSer 59

RESULT 14
US-10-898-408-12
; Sequence 12, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
; APPLICANT: GALIBERT, Laurent J.
; APPLICANT: YAN, Wei
; TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
; FILE REFERENCE: 3467-A
; CURRENT APPLICATION NUMBER: US/10/898,408
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/490,027
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-12
Alignment Scores:
Pred. No.: 0.00115 Length: 115
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 17 Gaps: 0

DELETED2 (1-81) x US-10-898-408-12 (1-115)
Qy 2 GGCGAGTCAGCATATTAGCAGCTGGTTAGCCGAATCAATCATAGTCGAAGCACCACCACT 61
Db 42 GlyLys----GlyLeu----GlutPrIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yrasnProSerLeuLysSer 65

RESULT 15
US-09-864-761-44315
; Sequence 44315, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rankel, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
```

```
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4315
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019439.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
; OTHER INFORMATION: EST HUMAN HIT: BE672445.1, EVALUE 2.00e-57
; OTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 1.00e-53
US-09-864-761-44315
```

```
Alignment Scores:
Pred. No.: 0.00115 Length: 117
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 9 Gaps: 0
```

DELETED2 (1-81) x US-09-864-761-44315 (1-117)

```
Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGAATCAATCATAGTGGAGCACCACACT 61
Db 45 GlyLys----GlyLeu----GluTrpIleGlyGluileAsnHisSerGlySerThrAsnT 62
Qy 62 ACAACCCCGCTCTCTCAAGAGT 81
Db 62 yAsnProSerLeuLysSer 68
```

Search completed: August 4, 2005, 20:23:29
Job time : 106.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:56:53 ; Search time 341.5 Seconds
(without alignments)
554.076 Million cell updates/sec

Title: DELETED2

Perfect score: 140

Sequence: 1 CGGGCGAGTCAGGATATTAG.....ACACCCGCTCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 13918532

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/NOLAN463-3b/runat_04082005_120455_19651/app_query.fasta_1.263
-DB=Pending_Patents_AA_Main -QFMT=fastan -SUFFIX=rapm -MINMATCH=0.1 -LOOPCPU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B @CGN 1 1 804 @runat_04082005_120455_19651 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG SCORES=0 -WALT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

Pending Patents AA Main:
1: /cgn2_6/ptodata/1/paa/pctus COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
14: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
15: /cgn2_6/ptodata/1/paa/US091 COMB.pcp.*
16: /cgn2_6/ptodata/1/paa/US092 COMB.pcp.*
17: /cgn2_6/ptodata/1/paa/US093 COMB.pcp.*
18: /cgn2_6/ptodata/1/paa/US094 COMB.pcp.*
19: /cgn2_6/ptodata/1/paa/US095 COMB.pcp.*
20: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
21: /cgn2_6/ptodata/1/paa/US097A COMB.pcp.*
22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
23: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*

29: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US105 COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
33: /cgn2_6/ptodata/1/paa/US107 COMB.pcp.*
34: /cgn2_6/ptodata/1/paa/US108 COMB.pcp.*
35: /cgn2_6/ptodata/1/paa/US109 COMB.pcp.*
36: /cgn2_6/ptodata/1/paa/US110 COMB.pcp.*
37: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------------------|--------------------|
| 1 | 104.4 | 74.6 | 124 | 22 | US-09-791-537-89288 | Sequence 89288, A |
| 2 | 102.1 | 72.9 | 125 | 22 | US-09-791-537-111128 | Sequence 111128, |
| 3 | 101.7 | 72.6 | 87 | 22 | US-09-791-537-144795 | Sequence 144795, |
| 4 | 101.7 | 72.6 | 125 | 22 | US-09-791-537-111072 | Sequence 111072, |
| 5 | 101.6 | 72.6 | 119 | 22 | US-09-791-537-716 | Sequence 716, App |
| 6 | 101.6 | 72.6 | 143 | 22 | US-09-791-537-36503 | Sequence 36503, A |
| 7 | 100.4 | 71.7 | 97 | 22 | US-09-791-537-78283 | Sequence 78283, A |
| 8 | 100.2 | 71.6 | 105 | 22 | US-09-791-537-22691 | Sequence 22691, A |
| 9 | 100.1 | 71.5 | 253 | 1 | PCT-US01-19110-1333 | Sequence 1333, Ap |
| 10 | 100.1 | 71.5 | 253 | 1 | PCT-US02-36496-1333 | Sequence 1333, Ap |
| 11 | 100.1 | 71.5 | 253 | 23 | US-09-880-748-1333 | Sequence 1333, Ap |
| 12 | 100.1 | 71.5 | 253 | 28 | US-10-293-418-1333 | Sequence 1333, Ap |
| 13 | 99.9 | 71.4 | 121 | 22 | US-09-791-537-110576 | Sequence 110576, |
| 14 | 99.9 | 71.4 | 125 | 1 | PCT-US03-05128-118 | Sequence 118, App |
| 15 | 99.9 | 71.4 | 125 | 29 | US-10-371-942-118 | Sequence 118, App |
| 16 | 98.7 | 70.5 | 119 | 22 | US-09-791-537-110532 | Sequence 110532, A |
| 17 | 98.7 | 70.5 | 130 | 22 | US-09-791-537-68863 | Sequence 68863, A |
| 18 | 98.2 | 70.1 | 67 | 22 | US-09-791-537-122614 | Sequence 122614, |
| 19 | 98.2 | 70.1 | 73 | 22 | US-09-791-537-134695 | Sequence 134695, |
| 20 | 98.2 | 70.1 | 80 | 26 | US-10-078-958-2 | Sequence 2, Appl |
| 21 | 98.2 | 70.1 | 88 | 22 | US-09-791-537-111396 | Sequence 111396, |
| 22 | 98.2 | 70.1 | 90 | 22 | US-09-791-537-130857 | Sequence 130857, |
| 23 | 98.2 | 70.1 | 91 | 22 | US-09-791-537-130896 | Sequence 130896, |
| 24 | 98.2 | 70.1 | 92 | 22 | US-09-791-537-130953 | Sequence 130953, |
| 25 | 98.2 | 70.1 | 92 | 22 | US-09-791-537-130969 | Sequence 130969, |
| 26 | 98.2 | 70.1 | 93 | 22 | US-09-791-537-151700 | Sequence 151700, |
| 27 | 98.2 | 70.1 | 93 | 22 | US-09-791-537-152140 | Sequence 152140, |
| 28 | 98.2 | 70.1 | 96 | 22 | US-09-791-537-152186 | Sequence 152186, |
| 29 | 98.2 | 70.1 | 97 | 1 | PCT-US02-22011-40 | Sequence 40, Appl |
| 30 | 98.2 | 70.1 | 97 | 1 | PCT-US02-38450-83 | Sequence 83, Appl |
| 31 | 98.2 | 70.1 | 97 | 1 | PCT-US03-06598-47 | Sequence 47, Appl |
| 32 | 98.2 | 70.1 | 97 | 12 | US-08-896-535-76 | Sequence 76, Appl |
| 33 | 98.2 | 70.1 | 97 | 19 | US-09-508-110-69 | Sequence 69, Appl |
| 34 | 98.2 | 70.1 | 97 | 22 | US-09-751-181-87 | Sequence 87, Appl |
| 35 | 98.2 | 70.1 | 97 | 22 | US-09-791-537-78284 | Sequence 78284, A |
| 36 | 98.2 | 70.1 | 97 | 22 | US-09-791-537-80274 | Sequence 80274, A |
| 37 | 98.2 | 70.1 | 97 | 22 | US-09-791-537-111367 | Sequence 111367, |
| 38 | 98.2 | 70.1 | 97 | 22 | US-09-791-537-126333 | Sequence 126333, |
| 39 | 98.2 | 70.1 | 97 | 22 | US-09-791-537-130951 | Sequence 130951, |
| 40 | 98.2 | 70.1 | 97 | 26 | US-10-029-3268-87 | Sequence 87, Appl |
| 41 | 98.2 | 70.1 | 97 | 26 | US-10-029-9888-87 | Sequence 87, Appl |
| 42 | 98.2 | 70.1 | 97 | 26 | US-10-032-0378-87 | Sequence 87, Appl |
| 43 | 98.2 | 70.1 | 97 | 26 | US-10-032-423A-87 | Sequence 87, Appl |
| 44 | 98.2 | 70.1 | 97 | 27 | US-10-189-258A-87 | Sequence 87, Appl |
| 45 | 98.2 | 70.1 | 97 | 27 | US-10-194-375-40 | Sequence 40, Appl |

ALIGNMENTS

RESULT 1
US-09-791-537-89288
; Sequence 89288, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.

```

; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89288
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-89288

Alignment Scores:
Pred. No.: 0.000343 Length: 124
Score: 104.40 Matches: 20
Percent Similarity: 45.28% Conservative: 3
Best Local Similarity: 37.74% Mismatches: 4
Query Match: 74.57% Indels: 26
DB: Gaps: 1

DELETED2 (1-81) x US-09-791-537-89288 (1-124)

Qy 1 CGGCGAGTCAGGATATTAGC----- 21
   :: |||::|||::|||
Db 13 LysLeuSerGluAspLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
Qy 22 -----AGCTGGTTAGCCGAAATCAAT 42
   |||:: |||::|||
Db 33 TyrTrpSerTrpIleArgAsgProGlyGlyLeuGluTrpIleGlyGluIleAsn 52
Qy 43 CATAGTCGAGCCCAACTACACCCGCTCTCAAGAGT 81
   |||:: |||::|||
Db 53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 2
US-09-791-537-111128
; Sequence 111128, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111128
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-111128

Alignment Scores:
Pred. No.: 0.000691 Length: 125
Score: 102.10 Matches: 21
Percent Similarity: 52.27% Conservative: 2
Best Local Similarity: 47.73% Mismatches: 2
Query Match: 72.93% Indels: 19
DB: Gaps: 1

DELETED2 (1-81) x US-09-791-537-111128 (1-125)

Qy 3 GCGCGAGTCAGGATATTAGC----- 21
   |||::|||::|||
Db 26 GlyGluSer----ValSerGlyTyrTyrTrpThrTrpIleArgGlnProProGlyLysG 44
Qy 22 ----AGCTGGTTAGCCGAAATCAATCATAGTGGAGGACCAACTACACCCGCTCTCAA 77
   |||::|||::|||

```

QY 9 TCAGGATATTAGC-----AGCTGTTAGC 32
Db 30 SerGlyTyr-SerTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleG1 49
QY 33 CGAATCAATCATAGTGAAGCACCACCACTACACCGCTCTCTCAAGAGT 81
Db 49 yGluIleAenHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 5
US-09-791-537-716
; Sequence 716, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 716
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-716

Alignment Scores:
Pred. No.: 0.000794 Length: 119
Score: 101.60 Matches: 19
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 67.86% Mismatches: 4
Query Match: 72.57% Indels: 4
DB: 22 Gaps: 0

DELETED2 (1-81) x US-09-791-537-716 (1-119)
QY 6 GAGTCAGCATATTAGCAGCTGGTTCAGCCCAATCAATCATAGTGAAGCACCACCACTACAA 65
Db 42 GluLysGlyLeu----GluTrpIleGlyGluIleAenHisSerGlySerThrAsnTyrAs 60
QY 66 CCCGCTCTCTCAAGAGT 81
Db 60 nProSerLeuLysSer 65

RESULT 6
US-09-791-537-36503
; Sequence 36503, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36503
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-36503

Alignment Scores:
Pred. No.: 0.000831 Length: 143
Score: 101.60 Matches: 19
Percent Similarity: 55.56% Conservative: 1
Best Local Similarity: 52.78% Mismatches: 2
Query Match: 72.57% Indels: 14

DB: 22 Gaps: 0
DELETED2 (1-81) x US-09-791-537-36503 (1-143)
QY 2 GGGCGAGTCAGGATATTAGCAGCTGGTTCAGCCCAATCAATCATAGTGAAGCACCACCACT 61
Db 44 GlyArg-----GluTrpIleGlyGluIleAenHisSerGlySerThrAsnT 59
QY 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yTrpSerLeuLysSer 65

RESULT 7
US-09-791-537-78283
; Sequence 78283, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78283
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-78283

Alignment Scores:
Pred. No.: 0.00109 Length: 97
Score: 100.40 Matches: 20
Percent Similarity: 43.40% Conservative: 3
Best Local Similarity: 37.74% Mismatches: 4
Query Match: 71.71% Indels: 26
DB: 22 Gaps: 1

DELETED2 (1-81) x US-09-791-537-78283 (1-97)
QY 1 CGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
QY 22 -----AGCTGTTAGCCCAATCAAT 42
Db 33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGlyGluIleAen 52
QY 43 CATAGTGAAGCACCACCACTACACCGCTCTCTCAAGAGT 81
Db 53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 8
US-09-791-537-22691
; Sequence 22691, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22691
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22691


```

Qy 3 GCGAGTCA-----CGATAT 17
Db 26 GlyGluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy 18 TAGCAGCTGGTTAGCGGAAATCAATCATAGTGGAGGACCACTACAACCGCTCTCTCAA 77
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy 78 GAGT 81
Db 64 sSer 65

RESULT 12
US-10-293-418-1333
; Sequence 1333, Application US/10293418
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1333

Alignment Scores:
Pred. No.: 0.00151 Length: 253
Score: 100.10 Matches: 21
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.73% Mismatches: 3
Query Match: 71.50% Indels: 19
DB: 28 Gaps: 1

DELETED2 (1-81) x US-10-293-418-1333 (1-253)

Qy 3 GCGAGTCA-----CGATAT 17
Db 26 GlyGluSerPheSerGlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 45

Qy 18 TAGCAGCTGGTTAGCGGAAATCAATCATAGTGGAGGACCACTACAACCGCTCTCTCAA 77
Db 46 ----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLy 64

Qy 78 GAGT 81
Db 64 sSer 65

RESULT 13
US-09-791-537-110576
; Sequence 110576, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek

```

```

; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 110576
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-110576

Alignment Scores:
Pred. No.: 0.00134 Length: 121
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 22 Gaps: 1

DELETED2 (1-81) x US-09-791-537-110576 (1-121)

Qy 3 GCGAGTCAGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerSerSerTyrTyrTrpGlyTrpIleArgGlnProProGl 44

Qy 25 -----TGGTTAGCGGAAATCAATCATAGTGGAGGACCACTACAACCGCTC 71
Db 44 YLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProse 64

Qy 72 TCTCAAGAGT 81
Db 64 rLeuLysSer 67

RESULT 14
PCT-US03-05128-118
; Sequence 118, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034WO1
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-118

Alignment Scores:
Pred. No.: 0.00135 Length: 125
Score: 99.90 Matches: 22
Percent Similarity: 50.00% Conservative: 1
Best Local Similarity: 47.83% Mismatches: 2
Query Match: 71.36% Indels: 21
DB: 1 Gaps: 1

DELETED2 (1-81) x PCT-US03-05128-118 (1-125)

Qy 3 GCGAGTCAGATATTAGCAGC----- 24
Db 26 GlyGlySer-----IleSerSerSerSerTyrTyrTrpAlaTrpIleArgGlnProProGl 44

Qy 25 -----TGGTTAGCGGAAATCAATCATAGTGGAGGACCACTACAACCGCTC 71
Db 44 YLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProse 64

```

Qy 72 TCTCAAGAGT 81
Db 64 rLeuLysSer 67

RESULT 15

```

US-10-371-942-118
; Sequence 118, Application US/10371942
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-118

```

| Alignment Scores: | |
|------------------------|---------|
| Pred. No.: | 0.00135 |
| Score: | 99.90 |
| Percent Similarity: | 50.00% |
| Best Local Similarity: | 47.83% |
| Query Match: | 71.36% |
| DB: | 29 |
| DB: | |
| Length: | 125 |
| Matches: | 22 |
| Conservative: | 1 |
| Mismatches: | 2 |
| Indels: | 21 |
| Gaps: | 1 |

DELETED2 (1-81) x US-10-371-942-118 (1-125)

| | | | | | | |
|----|----|------------|-----------|--------------|--------------|-------------------------------|
| Qy | 3 | GGCGAGT | CAGGATAT | TAGCAGC | ----- | 24 |
| | | | | | | |
| Db | 26 | GlyGlySer | ----- | IleSerSerSer | TyrTyrTyrAla | TrpIleArgGlnProProG1 44 |
| | | | | | | |
| Qy | 25 | ----- | TGGTTAGC | CGAATCA | TATCAT | TAGTGG |
| | | | | | | |
| Db | 44 | yLysGlyLeu | GluTrpIle | GlyGlu | LeuIleAsnHis | SerGlySerThrAsnTyrAsnProSe 64 |
| | | | | | | |
| Qy | 72 | TCTCAAG | AGT | 81 | | |
| | | | | | | |
| Db | 64 | rLeuLysser | 67 | | | |

Search completed: August 4, 2005, 20:18:16
Job time : 343.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:51:37 ; Search time 25 Seconds
(without alignments)
623.485 Million cell updates/sec

Title: DELETED2

Perfect score: 140

Sequence: 1 CGGCGAGTCAGGATATTAG.....ACAACCCGTCCTCTCAAGAGT 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPO_spool_p/NOLAN463-3B/runat_04082005_120454_19622/app_query.fasta_1.263
-DB=PIR -QWTF=fastcan -SUFFIX=rpr -MINMATCH=0.1 -LOPECL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=NOLAN463-3B@cgn 1.1.63 @runat_04082005_120454_19622 -NCPUs=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 101.6 | 72.6 | 143 | 2 | B49028 |
| 2 | 100.4 | 71.7 | 97 | 2 | S26805 |
| 3 | 98.2 | 70.1 | 97 | 2 | S26898 |
| 4 | 98.2 | 70.1 | 97 | 2 | S26806 |
| 5 | 98.2 | 70.1 | 106 | 2 | S37454 |
| 6 | 98.2 | 70.1 | 122 | 2 | JU0047 |
| 7 | 98.2 | 70.1 | 126 | 2 | S47010 |
| 8 | 98.2 | 70.1 | 140 | 2 | S78052 |
| 9 | 98.2 | 70.1 | 140 | 2 | A49045 |
| 10 | 98.2 | 70.1 | 231 | 2 | B23746 |
| 11 | 98 | 70.0 | 133 | 2 | P50341 |
| 12 | 94.2 | 67.3 | 97 | 2 | G34964 |
| 13 | 92 | 65.7 | 98 | 2 | S26905 |
| 14 | 92 | 65.7 | 145 | 2 | S78055 |

| | | | | | | |
|----|------|------|-----|---|--------|--------------------|
| 15 | 89.2 | 63.7 | 97 | 2 | S14474 | Ig heavy chain V r |
| 16 | 88 | 62.9 | 129 | 2 | S44114 | Ig heavy chain V r |
| 17 | 87.2 | 62.3 | 146 | 1 | G1HUH2 | Ig heavy chain pre |
| 18 | 86.2 | 61.6 | 134 | 2 | S54906 | Ig heavy chain V r |
| 19 | 86 | 61.4 | 98 | 2 | S26904 | Ig heavy chain V r |
| 20 | 83.7 | 59.8 | 134 | 2 | B24672 | Ig heavy chain pre |
| 21 | 83.2 | 59.4 | 114 | 2 | I72667 | cold agglutinin FS |
| 22 | 83 | 59.3 | 123 | 2 | S30529 | Ig heavy chain V r |
| 23 | 81.2 | 58.0 | 97 | 2 | JH0428 | Ig gamma chain V r |
| 24 | 80.3 | 57.4 | 116 | 2 | S38718 | Ig heavy chain V r |
| 25 | 80.1 | 57.2 | 98 | 2 | S26902 | Ig heavy chain V r |
| 26 | 80.1 | 57.2 | 98 | 2 | S12421 | Ig heavy chain V r |
| 27 | 80.1 | 57.2 | 130 | 2 | S31673 | Ig heavy chain V r |
| 28 | 80.1 | 57.2 | 140 | 2 | A24770 | hypothetical hybri |
| 29 | 79.9 | 57.1 | 127 | 2 | S19668 | Ig heavy chain V r |
| 30 | 79.1 | 56.5 | 97 | 2 | S26906 | Ig heavy chain V r |
| 31 | 79.1 | 56.5 | 97 | 2 | S12416 | Ig heavy chain V r |
| 32 | 79.1 | 56.5 | 105 | 2 | S44125 | Ig lambda chain V |
| 33 | 79.1 | 56.5 | 130 | 2 | S31690 | Ig heavy chain V r |
| 34 | 79.1 | 56.5 | 140 | 2 | I37782 | Ig variable region |
| 35 | 78.9 | 56.4 | 99 | 2 | S12412 | Ig heavy chain V r |
| 36 | 78.3 | 55.9 | 106 | 2 | S26464 | Ig heavy chain V r |
| 37 | 78.1 | 55.8 | 116 | 2 | B26340 | Ig heavy chain pre |
| 38 | 77.9 | 55.6 | 118 | 2 | A26340 | Ig heavy chain pre |
| 39 | 77.6 | 55.4 | 109 | 2 | PH1673 | Ig heavy chain V r |
| 40 | 77.2 | 55.1 | 97 | 2 | PL0118 | Ig heavy chain V-I |
| 41 | 77.2 | 55.1 | 99 | 2 | S26899 | Ig heavy chain V r |
| 42 | 77.2 | 55.1 | 130 | 2 | S30534 | Ig heavy chain V r |
| 43 | 77.1 | 55.1 | 97 | 2 | S26804 | Ig heavy chain V r |
| 44 | 77.1 | 55.1 | 97 | 2 | S26808 | Ig heavy chain V r |
| 45 | 77.1 | 55.1 | 116 | 2 | S18557 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

B49028

Ig heavy chain V-IV region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C/Accession: B49028

R/Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur

Eur. J. Immunol. 21, 2355-2363, 1991

A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob

A/Reference number: A49028; MUID:92008140; PMID:1915549

A/Accession: B49028

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-143 <TIM>

A/Cross-references: GB:S64473; NID:G236906; PIDN:AAB20012.1; PID:G236907

A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines

A/Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBI:64472)

A/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

| | | | | |
|------------------------|----------|---------------|-----|--|
| Alignment Scores: | | | | |
| Pred. No.: | 8.29e-05 | Length: | 143 | |
| Score: | 101.60 | Matches: | 19 | |
| Percent Similarity: | 55.56% | Conservative: | 1 | |
| Best Local Similarity: | 52.78% | Mismatches: | 2 | |
| Query Match: | 72.57% | Indels: | 14 | |
| DB: | 2 | Gaps: | 0 | |

DELETED2 (1-81) x B49028 (1-143)

Qy 2 GGGCGAGTCAGGATATTAGCTGGTTCAGCCGAAATCAATCATATAGTGGAGACCAACT 61

|||||

Db 44 GlyArg-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsn 59

Qy 62 ACAACCCGTCCTCAAGAGT 81

|||||

Db 59 yrAsnProSerLeuLysSer 65

```
RESULT 2
S26805
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26805
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26805
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WEN>
A:Cross-references: EMBL:Z14241; NID:g37714; PIDN:CAA78610.1; PID:g1335376
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000117 Length: 97
Score: 100.40 Matches: 20
Percent Similarity: 43.40% Conservatives: 3
Best Local Similarity: 37.74% Mismatches: 4
Query Match: 71.71% Indels: 26
DB: 2 Gaps: 1

DELETED2 (1-81) x S26805 (1-97)
Qy 1 CGGCGAGTCAGGATATTAGC----- 21
Db 13 LysProSerGlnThrLeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyr 32
Qy 22 -----AGCTGGTAGCCGAAATCAAT 42
Db 33 TyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIleGlyGluIleAsn 52
Qy 43 CATAGTCGAGCACCACCTACAAACCGCTCTCAAGAGT 81
Db 53 HisSerGlySerThrAsnTyrAsnProSerLeuLysSer 65

RESULT 3
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26898; S12420
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26898
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945
A:Experimental source: clone DP-63
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12420
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-97 <SAN>
A:Cross-references: EMBL:X56364
A:Experimental source: V(H)4.2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000228 Length: 97
```

```
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservatives: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x S26898 (1-97)
Qy 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACACT 61
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 4
S26806
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26806
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <WEN>
A:Cross-references: EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PID:g1335377
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000228 Length: 97
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservatives: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x S26806 (1-97)
Qy 2 GGCGGAGTCAGGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACACT 61
Db 42 GlyLys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 YrAsnProSerLeuLysSer 65

RESULT 5
S37454
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A:Reference number: S37453
A:Accession: S37454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <MCI>
A:Cross-references: EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PID:g758093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
```



```
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x S37454 (1-106)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
Db 20 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAent 37
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 37 yRAenProSerLeuLysSer 43

RESULT 6
JL0047
Ig heavy chain V region precursor (clone cR18) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C:Accession: JL0047
R:Baer, R.; Forster, A.; Lavenit, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new S
A:Reference number: JL0047; MUID:88258392; PMID:3133445
A:Accession: JL0047
A:Molecule type: mRNA
A:Residues: 1-122 <BAE>
A:Experimental source: T-cell line RPMI 8402
A:Note: The authors translated the reading frame which extends to the stop codon; the se
A:Note: this sequence belongs to the VH II subgroup
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00023 Length: 122
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x JL0047 (1-122)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
Db 50 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAent 67
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 67 yRAenProSerLeuLysSer 73

RESULT 7
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A:Reference number: S47009
A:Accession: S47010
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>
```

```
Alignment Scores:
Pred. No.: 0.00023 Length: 126
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x S47010 (1-126)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
Db 42 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAent 59
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 59 yRAenProSerLeuLysSer 65

RESULT 8
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Buraetero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and i
Patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X54441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.000231 Length: 140
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x S78052 (1-140)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACT 61
Db 56 GlyLys-----GlyLeu-----GluTrpIleGlyGluIleAsnHisSerGlySerThrAent 73
Qy 62 ACAACCCGCTCTCTCAAGAGT 81
Db 73 yRAenProSerLeuLysSer 79

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Rassenti, L.Z.; Labaume, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i b1
```

A;Reference number: A49045; MUID:92324290; PMID:1623923

A;Accession: A49045

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 <GR>

A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900

A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P:108089)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-116/Domain: immunoglobulin homology <IM>

Alignment Scores:
Pred. No.: 0.000231 Length: 140
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x A49045 (1-140)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61

Db 61 Glylys----GlyLeu----GlutrpiledGlyGluileAsnHisSerGlySerThrAsnT 78

Qy 62 ACAACCCGCTCTCTCAAGAGT 81

Db 78 yrAsnProSerLeuLysSer 84

RESULT 10

B23746 Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C;Accession: B23746

R;Leoni, J.; Ghiso, J.; Coni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A;Reference number: A23746; MUID:91131575; PMID:1993660

A;Accession: B23746

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-231 <LEO>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;140-209/Domain: immunoglobulin homology <IM>

Alignment Scores:
Pred. No.: 0.000236 Length: 231
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x B23746 (1-231)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61

Db 41 Glylys----GlyLeu----GlutrpiledGlyGluileAsnHisSerGlySerThrAsnT 58

Qy 62 ACAACCCGCTCTCTCAAGAGT 81

Db 58 yrAsnProSerLeuLysSer 64

RESULT 11

PS0341 Ig heavy chain V-D-J region (RAMOS) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-May-1997

C;Accession: PS0341

F;Ratech, H.

Biochem. Biophys. Res. Commun. 182, 1260-1263, 1992

A;Title: Rapid cloning of rearranged immunoglobulin heavy chain genes from human B-cell

A;Reference number: PS0341; MUID:92171937; PMID:1540170

A;Accession: PS0341

A;Molecule type: mRNA

A;Residues: 1-133 <RAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;9-38/Region: framework 1

F;39-43/Region: complementarity-determining 1

F;44-57/Region: framework 2

F;58-74/Region: complementarity-determining 2

F;75-106/Region: framework 3

Alignment Scores:
Pred. No.: 0.000245 Length: 133
Score: 98.00 Matches: 17
Percent Similarity: 94.74% Conservative: 1
Best Local Similarity: 89.47% Mismatches: 1
Query Match: 70.00% Indels: 0
DB: 2 Gaps: 0

DELETED2 (1-81) x PS0341 (1-133)

Qy 25 TGGTTAGCCGAAATCAATCATAGTGGAGGACCAACTACACCGTCTCTCAAGAGT 81

Db 55 TripiledGlyGluileAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSer 73

RESULT 12

G34964 Ig heavy chain V-IV region (Ab44) - human

C;Species: Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: G34964

R;Sanz, I.; Casali, P.; Thomas, J.W.; Nockins, A.L.; Capra, J.D.

J. Immunol. 142, 4054-4061, 1989

A;Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals ap

A;Reference number: A92830; MUID:89235232; PMID:2497188

A;Accession: G34964

A;Molecule type: mRNA

A;Residues: 1-97 <SAN>

A;Cross-references: UNIPROT:Q8WUX4; GB:M26998

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IM>

Alignment Scores:
Pred. No.: 0.000763 Length: 97
Score: 94.20 Matches: 18
Percent Similarity: 62.50% Conservative: 2
Best Local Similarity: 56.25% Mismatches: 4
Query Match: 67.29% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x G34964 (1-97)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGTTAGCCGAAATCAATCATAGTGGAGGACCAACT 61

Db 42 Glylys----GlyLeu----GlutrpiledGlyGluileAsnHisSerGlyGlyThrAsnT 59

Qy 62 ACAACCCGCTCTCTCAAGAGT 81

Db 59 yrAsnProSerLeuLysSer 65

RESULT 13

S26905 Ig heavy chain V region (DP-70 / 4.19) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S26905; S12419

R;Tomlinson, I.M.; WALTER, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26905

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <ROM>
A:Cross-references: EMBL:Z12370; NID:G32960; PIDN:CAA78240.1; PID:G32961
A>Note: designated DP-70
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12419
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <SAN>
A:Cross-references: EMBL:X56363
A>Note: designated 4.19
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00148 Length: 98
Score: 92.00 Matches: 21
Percent Similarity: 48.89% Conservativity: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1
DELETED2 (1-81) x S26905 (1-98)
Qy 3 GCGCAGTCAGGATATTAGCAGC----- 24
Db 26 GlyGlySer-----lleSerSerSerAsnTrpSerTrpValArgGlnProProGlyLy 44
Qy 25 -----TGGTTAGCGCGAAATCAATCATAGTGGAGACCACTAACACCGCTCTCT 74
Db 44 sGlyLeuGlutTrpIleGlyGluIleTyRHisSerGlySerThrAsnTyRAsnProSerLe 64
Qy 75 CAAGAGT 81
Db 64 uLySer 66

RESULT 14
S78055
Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78055; S23720
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78055
A:Molecule type: mRNA
A:Residues: 1-145 <HAR>
A:Cross-references: EMBL:X54445; NID:G37817; PIDN:CAA38312.1; PID:G37818
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Buraetero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23720
A:Molecule type: mRNA
A:Residues: 18-115 <HAW>
A:Cross-references: EMBL:X54445
A>Note: the authors translated the codon GCA for residue 67 as Arg
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00151 Length: 145
Score: 92.00 Matches: 21

Percent Similarity: 48.89% Conservativity: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1
DELETED2 (1-81) x S78055 (1-145)
Qy 3 GCGCAGTCAGGATATTAGCAGC----- 24
Db 43 GlyGlySer-----lleSerSerSerAsnTrpSerTrpValArgGlnProProGlyLy 61
Qy 25 -----TGGTTAGCGCGAAATCAATCATAGTGGAGACCACTAACACCGCTCTCT 74
Db 61 sGlyLeuGlutTrpIleGlyGluIleTyRHisSerGlySerThrAsnTyRAsnProSerLe 81
Qy 75 CAAGAGT 81
Db 81 uLySer 83

RESULT 15
S14474
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S14474
R:van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H.
submitted to the EMBL Data Library, November 1990
A:Reference number: S14474
A:Accession: S14474
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <ESJ>
A:Cross-references: EMBL:X56591; NID:G37235; PIDN:CAA39929.1; PID:G1335354
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 0.00345 Length: 97
Score: 89.20 Matches: 18
Percent Similarity: 62.50% Conservativity: 2
Best Local Similarity: 56.25% Mismatches: 4
Query Match: 63.71% Indels: 8
DB: 2 Gaps: 0
DELETED2 (1-81) x S14474 (1-97)

Qy 2 GCGCAGTCAGGATATTAGCAGCTGGTTAGCGCGAAATCAATCATAGTGGAGACCACT 61
Db 42 GlyLys-----GlyLeu----GlutTrpIleGlyGluIlelleHisSerGlySerThrAsn 59
Qy 62 ACAACCGCTCTCTCAAGAGT 81
Db 59 yrAsnProSerLeuLySer 65

Search completed: August 4, 2005, 20:05:40
Job time : 27 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: August 4, 2005, 19:40:06 ; Search time 116 Seconds
(without alignments)
715.145 Million cell updates/sec

Title: DELETED2

Perfect score: 140

Sequence: 1 CGGCGAGTCAGGATATTAG.....ACAACCCGTCCTCAAGAGT 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/NOLAN463-3B/runat.04082005.120453.19612/app.query.fasta_1.263
-DB=uniprot -OPMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCI=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=NOLAN463-3B @CGN 1.1 244 @runat.04082005.120453.19612 -NCPU=3
-NO.MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : Uniprot.03.*

1: uniprot.sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------|---------------------|
| 1 | 98.2 | 70.1 | 116 | 2 Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 2 | 98.2 | 70.1 | 595 | 2 Q8WUX4 | Q8WUX4 homo sapien |
| 3 | 98.2 | 70.1 | 597 | 2 Q8GMX5 | Q8GMX5 homo sapien |
| 4 | 98.2 | 70.1 | 597 | 2 Q9BU10 | Q9BU10 homo sapien |
| 5 | 98.2 | 70.1 | 625 | 2 Q96AA6 | Q96AA6 homo sapien |
| 6 | 92.2 | 65.9 | 597 | 2 Q9BQ88 | Q9BQ88 homo sapien |
| 7 | 92 | 65.7 | 576 | 2 Q5P418 | Q5P418 homo sapien |
| 8 | 87.2 | 62.3 | 146 | 1 HV2I1 HUMAN | P06331 homo sapien |
| 9 | 82.1 | 58.6 | 477 | 2 Q8GMX7 | Q8GMX7 homo sapien |
| 10 | 79.1 | 56.5 | 139 | 2 Q86SX2 | Q86SX2 homo sapien |
| 11 | 77.1 | 55.1 | 620 | 2 Q96EY0 | Q96EY0 homo sapien |
| 12 | 76.3 | 54.5 | 479 | 2 Q99M22 | Q99M22 mus musculus |
| 13 | 75.7 | 54.1 | 116 | 1 HV61 MOUSE | P18532 mus musculus |
| 14 | 75.2 | 53.7 | 465 | 2 Q8GMX6 | Q8GMX6 homo sapien |
| 15 | 72.8 | 52.0 | 262 | 2 Q5Z11 | Q5Z11 mus musculus |
| 16 | 71.3 | 50.9 | 116 | 1 HV60_MOUSE | P18531 mus musculus |

| | | | | | |
|----|------|------|-----|--------------|---------------------|
| 17 | 71.2 | 50.9 | 119 | 2 Q9UL73 | Q9UL73 homo sapien |
| 18 | 71.2 | 50.9 | 476 | 2 Q6GMX1 | Q6GMX1 homo sapien |
| 19 | 69.1 | 49.4 | 478 | 2 Q6NYH3 | Q6NYH3 homo sapien |
| 20 | 68.6 | 49.0 | 150 | 2 Q95973 | Q95973 homo sapien |
| 21 | 68.2 | 48.7 | 478 | 2 Q7Z379 | Q7Z379 homo sapien |
| 22 | 67.4 | 48.1 | 113 | 1 HV47_MOUSE | P01823 mus musculus |
| 23 | 66.4 | 47.4 | 104 | 2 Q99CA9 | Q99CA9 human immun |
| 24 | 66.4 | 47.4 | 106 | 2 Q6TU04 | Q6TU04 human immun |
| 25 | 65.9 | 47.4 | 133 | 2 Q90QV6 | Q90QV6 human immun |
| 26 | 65.9 | 47.1 | 496 | 2 Q96KX8 | Q96KX8 homo sapien |
| 27 | 65.5 | 46.8 | 523 | 2 Q6QJ60 | Q6QJ60 paraphlegop |
| 28 | 65.5 | 46.8 | 523 | 2 Q6QJ62 | Q6QJ62 paraphlegop |
| 29 | 65.4 | 46.7 | 104 | 2 Q99CH3 | Q99CH3 human immun |
| 30 | 65.4 | 46.7 | 130 | 2 Q9QL43 | Q9QL43 human immun |
| 31 | 65.4 | 46.7 | 202 | 2 Q9IUP1 | Q9IUP1 human immun |
| 32 | 65.4 | 46.7 | 202 | 2 Q9IUR6 | Q9IUR6 human immun |
| 33 | 65.4 | 46.7 | 206 | 2 Q7Z97 | Q7Z97 human immun |
| 34 | 65.4 | 46.7 | 207 | 2 Q9IU05 | Q9IU05 human immun |
| 35 | 65.4 | 46.7 | 212 | 2 Q9J783 | Q9J783 human immun |
| 36 | 65.4 | 46.7 | 220 | 2 Q9IUT6 | Q9IUT6 human immun |
| 37 | 65.4 | 46.7 | 231 | 2 Q9IQS9 | Q9IQS9 human immun |
| 38 | 65.4 | 46.7 | 489 | 2 Q80632 | Q80632 human immun |
| 39 | 65.3 | 46.6 | 136 | 2 Q6LBO5 | Q6LBO5 mus musculus |
| 40 | 65.3 | 46.6 | 137 | 1 HV46_MOUSE | P01822 mus musculus |
| 41 | 64.4 | 46.0 | 130 | 2 Q7ZB82 | Q7ZB82 human immun |
| 42 | 64.4 | 46.0 | 131 | 2 Q90Q75 | Q90Q75 human immun |
| 43 | 64.4 | 46.0 | 131 | 2 Q9QKY2 | Q9QKY2 human immun |
| 44 | 64.4 | 46.0 | 131 | 2 Q9QKY3 | Q9QKY3 human immun |
| 45 | 64.4 | 46.0 | 140 | 2 Q69828 | Q69828 human immun |

ALIGNMENTS

RESULT 1
Q7Z3Y6 PRELIMINARY; PRT; 116 AA.
ID Q7Z3Y6;
AC Q7Z3Y6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN Name=VH4-34;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauninger A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -
DR HSSP; P18532; 1KCV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12902 MW; CE3D8A846616C908 CRC64;

Alignment Scores:
Pred. No.: 0.000436 Length: 116
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q7Z3Y6 (1-116)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGTTAGCGGAATCAATCATAGTGGAGACCAACT 61

```
||||:| 42 GlyLys---GlyLeu---GluTrpIleGlyGluIleAenHisSerGlySerThrAsnT 59
||||:| 62 ACAACCCGTCCTCAAGAGT 81
||||:| 59 YrAsnProSerLeuLysSer 65

RESULT 2
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Alignment Scores:
Pred. No.: 0.000538 Length: 595
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q8WUX4 (1-595)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCGCGAAATCAATCATAGTCGAAGCACCACACT 61
Db 68 GlyLys---GlyLeu---GluTrpIleGlyGluIleAenHisSerGlySerThrAsnT 85
```

```
||||:| 62 ACAACCCGTCCTCAAGAGT 81
||||:| 85 YrAsnProSerLeuLysSer 91

RESULT 3
Q6GMX5 PRELIMINARY; PRT; 597 AA.
AC Q6GMX5
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Alignment Scores:
Pred. No.: 0.000538 Length: 597
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q6GMX5 (1-597)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCGCGAAATCAATCATAGTCGAAGCACCACACT 61
```

```

Db 61 GlyLys-----GlyLeu-----GlutrpIleGlyGuileAsnHisSerGlySerThrAsnT 78
Qy 62 AACACCCGCTCTCTCAAGAGT 81
Db 78 YrAsnProSerLeuLysSer 84

RESULT 4
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Alignment Scores:
Pred. No.: 0.000538 Length: 597
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q9BU10 (1-597)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGGAATCATATAGTGGAGCCCAACT 61
Db 61 GlyLys-----GlyLeu-----GlutrpIleGlyGuileAsnHisSerGlySerThrAsnT 78

```

```

Qy 62 AACACCCGCTCTCTCAAGAGT 81
Db 78 YrAsnProSerLeuLysSer 84

RESULT 5
ID Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; FG2FAB3ADE7ECBFE CRC64;

Alignment Scores:
Pred. No.: 0.000541 Length: 625
Score: 98.20 Matches: 19
Percent Similarity: 65.62% Conservative: 2
Best Local Similarity: 59.38% Mismatches: 3
Query Match: 70.14% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q96AA6 (1-625)

Qy 2 GGGCGAGTCAGGATATTAGCAGCTGGTTAGCCGGAATCATATAGTGGAGCCCAACT 61

```

```
||||:| 68 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 85
||||:| 62 ACAACCGCTCTCTCAAGAGT 81
||||:| 85 yzAsnProSerLeuLysSer 91

RESULT 6
Q9BQB8 PRELIMINARY; PRT; 597 AA.
ID Q9BQB8
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHD protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AA06180.1; -.
DR HSSP; P01861; 1AQO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:
Pred. No.: 0.00355 Length: 597
Score: 92.20 Matches: 18
Percent Similarity: 62.50% Conservative: 2
Best Local Similarity: 56.25% Mismatches: 4
Query Match: 65.86% Indels: 8
DB: 2 Gaps: 0

DELETED2 (1-81) x Q9BQB8 (1-597)

Qy 2 GGGCGAGTCAGATATTAGCAGCTGGTTAGCCGAAATCAATCATAGTGGAGACCAACT 61
Db 61 Glylys----GlyLeu----GluTrpIleGlyGluIleAsnHisSerGlySerThrAsnT 78
||||:|
```

```
62 ACAACCGCTCTCTCAAGAGT 81
||||:| 78 yzAsnProSerLeuLysSer 84

RESULT 7
Q6P4I8 PRELIMINARY; PRT; 576 AA.
ID Q6P4I8
AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
CN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; PBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 0.00377 Length: 576
Score: 92.00 Matches: 21
Percent Similarity: 48.89% Conservative: 1
Best Local Similarity: 46.67% Mismatches: 3
Query Match: 65.71% Indels: 20
DB: 2 Gaps: 1

DELETED2 (1-81) x Q6P4I8 (1-576)
```



```

Qy 3 GGCAGTCAGCATATTAGCAGC-----24
D 52 GlyGlySer-----IleSerSerSerSerTrpValArgGlnProProGlyLy 70
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCT 74
D 70 sGlyLeuGluTrpIleGlyGlyIleTyHiseSerGlySerThrAsnTyHseProSerLe 90
Qy 75 CAAGAGT 81
D 90 uLySer 92

RESULT 8
HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 39, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=8520332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR; A02101; GI1042.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Alignment Scores:
Pred. No.: 0.0143 Length: 146
Score: 87.20 Matches: 18
Percent Similarity: 59.38% Conservative: 1
Best Local Similarity: 56.25% Mismatches: 5
Query Match: 62.29% Indels: 8
DB: 1 Gaps: 0

DELETED2 (1-81) x HV21_HUMAN (1-146)

Qy 2 GGCAGTCAGCATATTAGCAGTCGGTTAGCCGAAATCAATCATAGTGGAGCACCACCACT 61
D 62 GlyArg---GlyLeu---GluTrpIleGlyGlyIleAsnHiseSerGlySerThrAsnT 79
Qy 62 ACAACCGCTCTCTCAAGAGT 81
D 79 yrLysThrSerLeuLySer 85

RESULT 9
Q6GMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7
AC Q6GMX7;

```

```

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00407; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Alignment Scores:
Pred. No.: 0.0828 Length: 477
Score: 82.10 Matches: 19
Percent Similarity: 47.73% Conservative: 2
Best Local Similarity: 43.18% Mismatches: 4
Query Match: 58.64% Indels: 19
DB: 2 Gaps: 1

DELETED2 (1-81) x Q6GMX7 (1-477)

Qy 3 GGCAGTCAGCATATTAGCAGC-----24
D 45 GlyGlySer-----IleSerSerTyTrpSerTrpIleArgGlnThrAlaGlyLyG 63
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGAGCACCACCACTACACCGTCTCTCAA 77
D 63 yLeuGluTrpIleGlyTyHiseSerGlySerGlySerThrTyHseProSerLeuLy 83
Qy 78 GAGT 81

```

```

Db      83 sSer 84
RESULT 10
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2
ID Q86SX2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSDDL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL EMBL; BX248300; CAD62627.1; -.
DR HSPF; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
FT NON TER
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Alignment Scores:
Pred. No.: 0.182 Length: 139
Score: 79.10 Matches: 19
Percent Similarity: 47.73% Conservative: 2
Best Local Similarity: 43.18% Mismatches: 4
Query Match: 56.50% Indels: 19
DB: 2 Gaps: 1

DELETED2 (1-81) x Q86SX2 (1-139)
Qy 3 GCGGAGTCAGATATTAGCAGC----- 24
Db 58 GlyGlySer-----IleSerSerTyrTrpSerTrpIleArgGlnProProGlyLysG1 76
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACCGTCTCTCAA 77
Db 76 yLeuGlutTrpIleGlyTyrIleTyrSerGlySerThrAsnTrpAsnProSerLeuLy 96
Qy 78 GAGT 81
Db 96 sSer 97

RESULT 11
Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
ID Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

```

```

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
RP and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSPF; P01820; IG7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Alignment Scores:
Pred. No.: 0.413 Length: 620
Score: 77.10 Matches: 19
Percent Similarity: 45.45% Conservative: 1
Best Local Similarity: 43.18% Mismatches: 5
Query Match: 55.07% Indels: 19
DB: 2 Gaps: 1

DELETED2 (1-81) x Q96EY0 (1-620)
Qy 3 GCGGAGTCAGATATTAGCAGC----- 24
Db 52 GlyGlySer-----IleSerSerTyrTrpSerTrpIleArgGlnProLaGlyLysG1 70
Qy 25 -----TGGTTAGCCGAAATCAATCATAGTGGAGCACCACCAACCGTCTCTCAA 77
Db 70 yLeuGlutTrpIleGlyTyrIleTyrSerGlySerThrAsnTrpAsnProSerLeuLy 90
Qy 78 GAGT 81
Db 90 sSer 91

RESULT 12
Q99M22 PRELIMINARY; PRT; 479 AA.
ID Q99M22
AC Q99M22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.W., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RC Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC02091; AA02091.1; -;
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 5192 MW; 768E39A138918892 CRC64;

Alignment Scores:
Pred. No.: 0.513 Length: 479
Score: 76.30 Matches: 15
Percent Similarity: 37.04% Conservative: 5
Best Local Similarity: 27.78% Mismatches: 27
Query Match: 54.50% Indels: 27
DB: 2 Gaps: 1

DELETED2 (1-81) x Q99M22 (1-479)
Qy 1 CGGGCGATCAGGATATTAGC----- 21
Db 31 LysProSerGinSerLeuSerLeuThrCysSerValThrGlyTyrSerIleThrSerGly 50
Qy 22 -----AGCTGGTACCGGAAATC 39
Db 51 TyrTyrTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetGlyTyrIle 70
Qy 40 AATCATAGTGAAGACCACTACAAACCCGCTCTCTCAAGAGT 81
Db 71 AsnTyrAspGlySerAsnAsnTyrAsnProSerLeuLysAsn 84

RESULT 13
ID HV61 MOUSE
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/cJ;
RC MEDLINE=89279149; PubMed=2499654;
RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
DR FIR; JT0508; HVMS1B.
DR PDB; 1KCS; X-ray; H=19-116.
DR PDB; 1KCV; X-ray; H=19-116.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 Ig heavy chain V region 1B43.
FT DOMAIN 19 48 Framework-1.
FT DOMAIN 49 53 Complementarity-determining-1.
FT DOMAIN 54 67 Framework-2.
FT DOMAIN 68 84 Complementarity-determining-2.
FT DOMAIN 85 116 Framework-3.
FT DISULFID 40 114 By similarity.
FT STRAND 21 25
FT STRAND 29 30
FT TURN 32 33
FT STRAND 36 43
FT TURN 47 49
FT TURN 52 58
FT TURN 60 61
FT TURN 64 71
FT TURN 72 73
FT STRAND 76 78
FT TURN 80 85
FT STRAND 86 91
FT TURN 92 95
FT STRAND 96 101
FT HELIX 106 108
FT STRAND 110 116
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Alignment Scores:
Pred. No.: 0.517 Length: 116
Score: 75.70 Matches: 16
Percent Similarity: 56.76% Conservative: 5
Best Local Similarity: 43.24% Mismatches: 3
Query Match: 54.07% Indels: 13
DB: 1 Gaps: 1

DELETED2 (1-81) x HV61_MOUSE (1-116)
Qy 9 TCAGGATATTAGC-----AGCTGGTATTAGC 32
Db 49 SerGlyTyr-SerTrpHisTrpIleArgGlnPheProGlyAsnLysLeuGluTrpMetG1 68
Qy 33 CGAATCAATCATAGTGAAGCACCACTACAAACCCGCTCTCTCAAGAGT 81
Db 68 yTyrIleHisTyrSerGlyAsnThrSerTyrAsnProSerLeuLysSer 84

RESULT 14
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```

